

CD4: 55%

>ref|NP_000607.1| CD4 antigen precursor [Homo sapiens]

Length=458

GENE ID: 920 CD4 | CD4 molecule [Homo sapiens] (Over 100 PubMed links)

Score = 459 bits (1181), Expect = 2e-129

Identities = 249/450 (55%), Positives = 314/450 (69%), Gaps = 8/450 (1%)

Query 9 rllllllqlsqliAVTQCKTLVLGKEGESAELPCESSQKKITVFTWKFSDQRKILGQH GK 68
R LLL+LQL+ L A TQCK +VLGK+G++ EL C +SQKK F WK S+Q KILG G
Sbjct 8 RHLLLVQLLALLPAATQCKKVVLGKGDVELTCTASQKKSIQFHWKNSNQIKILGNQGS 67

Query 69 GVLIRGGSPSQFDRFDSKKGAWEKGSFPLIINKLKMEDSQTYYICELENRKEEVELWVFKV 128
+ G DR DS++ W++G+FPLII LK+EDS TYICE+E++KEEV+L VF +
Sbjct 68 --FLTkgPSKLNDRADSRRLWDQGNFPLIINKLKIEDSDTYICEVEDQKEEVQLLVFGL 125

Query 129 TFSpgtsllqgqsltltlDSNSKVSNNPLTECKHkkgkvvsqskvLSMSNLRVQDSDFWNC 188
T + T LLQGGSLTLTL+S S+P +C+ +GK + G K LS+S L +QDS W C
Sbjct 126 TANSdTHLLQGGSLTLTLSPPG-SSPSVQCRSPRGKNIQGGKTLVSQLELQDSGTWTC 184

Query 189 TVTLDQKKNWFGMTLSVLGFQSTAITAYKSEGESAIEFSFPLNFAEEN--GWGELMWKA EK 246
TV +QKK F + + VL FQ + YK EGE EFSFPL F E G GEL W+AE+
Sbjct 185 TVLQNKQKVEFKIDIVLAFQKASSIVYKKEGEQVEFSFPLAFTVEKLTGSGELWWQAER 244

Query 247 DSFFQPWISFSIKNKEVSVQKSTKDLKLQLKETLPLTLKIPQVSLQFAGSGNLTLDK- 305
S + WI+F +KNKEVSV++ T+D KLQ+ + LPL L +PQ Q+AGSGNLT L+
Sbjct 245 ASSSKSWITFDLKNKEVSVKRVTDQPKLQMGKKLPLHLTLPLQALPQYAGSGNLTALAEAK 304

Query 306 -GTLHQEVNVLVVMKVAQLNNTLTCEVMGPTSPKMRLTLKQENQEARVSEEQKVQVVAPE 364
G LHQEVNVLVM+ QL LTCEV GPTSPK+ L+LK EN+EA+VS+ +K V V+ PE
Sbjct 305 TGKLHQEVNVLVVMRATQLQKNLTCEVWGPTSPKLMLSLKLENKAKVSKREKAVVVLNPE 364

Query 365 TGLWQCLLSEGDVKMDSRIQVLSRGVNQTVFLA-CVlggsfgflgflglcilccVRCRH 423
G+WQCLLS+ +V ++S I+VL +A VLGG G L F+GL I CVRCRH
Sbjct 365 AGMWQCLLSDSGQVLLESNIKVLPTWSTPVQPMALIVLGGVAGLLLFIGLGIFFCVRCRH 424

Query 424 QQRQAARMSQIKRLLSEKKTQCPCPHRMQKS 453
++RQA RMSQIKRLLSEKKTQCPCPHR QK+
Sbjct 425 RRRQAARMSQIKRLLSEKKTQCPCPHRFQKT 454



Her2: 87%

GENE ID: 2064 ERBB2 | v-erb-b2 erythroblastic leukemia viral oncogene homolog
2, neuro/glioblastoma derived oncogene homolog (avian) [Homo sapiens]
(Over 100 PubMed links)

Score = 2308 bits (5981), Expect = 0.0

Identities = 1101/1256 (87%), Positives = 1156/1256 (92%), Gaps = 1/1256 (0%)

Query	1	MELAAWCRWGFLLALLSPGAAGTQVCTGTDMLRLPASPETHDMLRHLYQGCQVVGQNL	60
		MELAA CRWG LLALL PGAA TQVCTGTDMLRLPASPETHDMLRHLYQGCQVVGQNL	
Sbjct	1	MELAALCRWGLLLALLPPGAASTQVCTGTDMLRLPASPETHDMLRHLYQGCQVVGQNL	60
Query	61	ELTYLPANASLSFLQDIQEVQGYMLIAHNRVKHVPLQRLRIVRGTLFEDKYALAVLDNR	120
		ELTYLP NASLSFLQDIQEVQGY+LIAHN+V+ VPLQRLRIVRGTLFED YALAVLDN	
Sbjct	61	ELTYLPTNASLSFLQDIQEVQGYVLIAHNQVRQVPLQRLRIVRGTLFEDNYALAVLDNG	120
Query	121	DPLDNVTTAAPGRTPPEGLRELQLRSLTEILKGGVLI RGNPQLCYQDMVLWKDVL RKNQNL	180
		DPL+N TT G +P GLRELQLRSLTEILKGGVLI+ NPQLCYQD +LWKD+ KNNQL	
Sbjct	121	DPLNN-TTPVTGASPGGLRELQLRSLTEILKGGVLIQRNPQLCYQDTILWKDIFHKNNQL	179
Query	181	APVMDTNRSRACPPCAPTCKDNHCWGESPEDCQILTGTICTSGCARCKGRLPTDCCHEQ	240
		A +DTNRSRAC PC+P CK + CWGES EDCQ LT T+C GCARCKG LPTDCCHEQ	
Sbjct	180	ALTLDITNRSRACHPCSPMCKGSRWCWGESSEDCQSLTRTVCAGGCARCKGPLPTDCCHEQ	239
Query	241	CAAGCTGPKHSDCLACLHFNHSGICELHCPALITYNTDTFESMLNPEGRYTFGASCVTTC	300
		CAAGCTGPKHSDCLACLHFNHSGICELHCPAL+TYNTDTFESM NPEGRYTFGASCVT C	
Sbjct	240	CAAGCTGPKHSDCLACLHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTAC	299
Query	301	PYNYLSTEVGSCCTLVCPNNQEVTAEDGTQRCEKCSKPCAGVCYGLGMEHLRGARAITSD	360
		PYNYLST+VGSCCTLVCP +NQEVTAEDGTQRCEKCSKPCA VCYGLGMEHLR RA+TS	
Sbjct	300	PYNYLSTDVGSCCTLVCPLNHNEVTAEDGTQRCEKCSKPCARVCYGLGMEHLREVRAVTS	359
Query	361	NIQEFAGCKKIFGSLAFLPESFDGNPSSGVAPLKPEHLQVFETLEEITGYLYISAWPESF	420
		NIQEFAGCKKIFGSLAFLPESFDG+P+S APL+PE LQVFETLEEITGYLYISAWP+S	
Sbjct	360	NIQEFAGCKKIFGSLAFLPESFDGDPASNTAPLQPEQLQVFETLEEITGYLYISAWPDSL	419
Query	421	QDLSVFQNLVRIGRILHDGAYSLTLQGLGIHslglrsrlrelgsglaliHRNTHLCFVNT	480
		DLSVFQNL+VIRGRILH+GAYSLTLQGLGI LGLRSLRELGSGLALIH NTHLCFV+T	
Sbjct	420	PDLSVFQNLQVIRGRILHNGAYSLTLQGLGISWLGLRSLRELGSGLALIHNNTHLCFVHT	479
Query	481	VPWDQLFRNPHQALLHSGNRPEEACGLEGLVCNSLCARGHCWGPGPTQCVNCSQFLRGQE	540
		VPWDQLFRNPHQALLH+ NRPE+ C EGL C+ LCARGHCWGPGPTQCVNCSQFLRGQE	
Sbjct	480	VPWDQLFRNPHQALLHTANRPEDECVGEGLACHQLCARGHCWGPGPTQCVNCSQFLRGQE	539
Query	541	CVEECRVWKGLPREYVRGKHCLPCHPECQPQNSSETCYGSEADQCEACAHYKDSSECVAR	600
		CVEECRV +GLPREYV +HCLPCHPECQPQN S TC+G EADQC ACAHYKD CVAR	
Sbjct	540	CVEECRVLQGLPREYVNARHCLPCHPECQPQNGSVTCFGPEADQCVACAHYKDPFCVAR	599
Query	601	CPSGVKPDLSYMPIWKYPDEEGICQPCPINCTHSCVDLDERGCPAEQRASPVTFIIATvv	660
		CPSGVKPDLSYMPIWK+PDEEG CQPCPINCTHSCVDLD++GCPAEQRASP+T II+ VV	
Sbjct	600	CPSGVKPDLSYMPIWKFPDEEGACQPCPINCTHSCVDLDDKGCPAEQRASPLTSIISAVV	659
Query	661	gvllfliivvvigilikrrrqkirkYTMRRLLQETELVEPLTPSGAVPNQAQMRIKETE	720

Sbjct	660	G+LL +++ VV GILIKRR+QKIRKYTMRRLLQETELVEPLTPSGA+PNQAQMRILKETE GILLVVVLGVVFGILIKRRQKIRKYTMRRLLQETELVEPLTPSGAMPNQAQMRILKETE	719
Query	721	LRKLKVLGSGAFGTVYKGIWIPDGENVKIPVAIKVLENTSPKANKEILDEAYVMAGVGS LRK+KVLGSGAFGTVYKGIWIPDGENVKIPVAIKVLENTSPKANKEILDEAYVMAGVGS	780
Sbjct	720	LRKVVLGSGAFGTVYKGIWIPDGENVKIPVAIKVLENTSPKANKEILDEAYVMAGVGS	779
Query	781	PYVSRLLGICLTSTVQLVTQLMPYGCLLDHVREHGRGLGSQDLLNWCVQIAKMSYLEEV PYVSRLLGICLTSTVQLVTQLMPYGCLLDHVRE+RGRLGSQDLLNWC+QIAKMSYLE+V	840
Sbjct	780	PYVSRLLGICLTSTVQLVTQLMPYGCLLDHVRENRGRLGSQDLLNWCQIAKMSYLEDV	839
Query	841	RLVHRDLAARNVLKSPNHVKITDFGLARLLDIDETEHADGGKVPIKWMALLESILRRRF RLVHRDLAARNVLKSPNHVKITDFGLARLLDIDETEHADGGKVPIKWMALLESILRRRF	900
Sbjct	840	RLVHRDLAARNVLKSPNHVKITDFGLARLLDIDETEHADGGKVPIKWMALLESILRRRF	899
Query	901	THQSDVWSYGVTVWELMTFGAKPYDGIPAREIPDLLEKGERLPQPPICTIDVYIMVVKCW THQSDVWSYGVTVWELMTFGAKPYDGIPAREIPDLLEKGERLPQPPICTIDVYIMVVKCW	960
Sbjct	900	THQSDVWSYGVTVWELMTFGAKPYDGIPAREIPDLLEKGERLPQPPICTIDVYIMVVKCW	959
Query	961	MIDSECRPRFRELVSFMRMARDPQRFVVIQNEDLGPSSPMDSTFYRSLEDDDMGELVD MIDSECRPRFRELVSFMRMARDPQRFVVIQNEDLGP+SP+DSTFYRSLEDDDMG+LVD	1020
Sbjct	960	MIDSECRPRFRELVSFMRMARDPQRFVVIQNEDLGPASPLDSTFYRSLEDDDMGDLVD	1019
Query	1021	AEEYLVPQQGFFSPDPALGtgstahrrhrssarsgggeltlglepseepprsplapse AEEYLVPQQGFF PDPA G G H RHRSSS RSGGG+LTGLGPSEEE PRSPLAPSE	1080
Sbjct	1020	AEEYLVPQQGFFCPDPAPGAGGMVHHRSSSTRSGGGDLTGLGPSEEEAPRSPLAPSE	1079
Query	1081	GAGSDVFDGDLAVGVTKGLQSLSPHDLSPQRYSEDPTLPLPETDGYVAPLACSPQPEY GAGSDVFDGDL +G KGLQSL HD SPLQRYSEDPT+PLP ETDGYVAPL CSPQPEY	1140
Sbjct	1080	GAGSDVFDGDLGMGAAGLQSLPTHDPSPQRYSEDPTVPLPSETDGYVAPLTCSPQPEY	1139
Query	1141	VNQPEVRpqspltpgppppirpAGATLERPKTLPKGKNGVVKDVFAFGGAVENPEYLAP VNQP+VRPQ P EGP P RPAGATLERPKTLPKGKNGVVKDVFAFGGAVENPEYL P	1200
Sbjct	1140	VNQPDVRPQPPSPREGPLPAARPAGATLERPKTLPKGKNGVVKDVFAFGGAVENPEYLTP	1199
Query	1201	RAGTASQPHPSPAFSPAFDNLYYWDQNSSEQGPPPPSTFEGTPTAENPEYLGLDVPV + G A QPHP PAFSPAFDNLYYWDQ+ E+G PPSTF+GTPTAENPEYLGLDVPV	1256
Sbjct	1200	QGGAAPQPHPPAFSPAFDNLYYWDQDPPERGAPPSTFKGTPTAENPEYLGLDVPV	1255

CD80: 45%

>ref|NP_005182.1| CD80 antigen precursor [Homo sapiens]

Length=288

GENE ID: 941 CD80 | CD80 molecule [Homo sapiens] (Over 10 PubMed links)

Score = 228 bits (581), Expect = 5e-60

Identities = 124/271 (45%), Positives = 171/271 (63%), Gaps = 6/271 (2%)

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Query 18  CPrlillfvllir-LSQVSSDVDEQLSKSVKDKVLLPCRYNSPHEDESEDRIYWQKHDKV 76
          CP L   +L++ LS  S V  ++K VK+  L C +N  E+ ++ RIYWQK  K+
Sbjct 14  CPYLNFFQLLVLAGLSHFCSGVIH-VTKEVKEVATLSCGHNVSV EELAQTRIYWQKEKKM 72

Query 77  VLSVIAGKLVWPEYKNRTLYDNTT-YSLIILGLVLSDRGTYS CVVQKKERGTYEVKHLA 135
          VL+++G + +WPEYKNRT++D T  S++IL L  SD GTY CVV K E+  ++ +HLA
Sbjct 73  VLTMMSGDMNIWPEYKNRTIFDITNNLSIVILALRPSDEGTYESCVVLKYEKDAFKREHLA 132

Query 136 LVKLSIKADFSTPNITESGNPSADTKRITCFASGGFPKPRFSWLENGRELPGINTTISQD 195
          V LS+KADF TP+I++  P+++ +RI C  SGGFP+P  SWLENG EL  INTT+SQD
Sbjct 133 EVTLSVKADFPTPSISDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQD 192

Query 196 PESELYTISSQLDFNTTRNHTIKCLIKYGDAHVSEDFTWEKPPEDP-PDSKNTLVLFAGAG 254
          PE+ELY +SS+LDFN T NH+ CLIKYG  V++ F W  ++ PD N L  +
Sbjct 193 PETELYAVSSKLDNMTTNHSMCLIKYGHLRVNQTFNWNNTTKQEHFPD--NLLPSWAIT 250

Query 255 FGAvitvvviiKCFCKHRSCFRRNEASR 285
          +V + VI + CF      RRNE R
Sbjct 251 LISVNGIFVICCLTYCFAPRCRERRRNERLR 281
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CD86: 50%

>ref|NP_787058.3| CD86 antigen isoform 1 [Homo sapiens]

Length=329

GENE ID: 942 CD86 | CD86 molecule [Homo sapiens] (Over 10 PubMed links)

Score = 287 bits (734), Expect = 9e-78

Identities = 154/305 (50%), Positives = 198/305 (64%), Gaps = 9/305 (2%)

```
Query 1 MDPRCTMGLAILIFVTVLLISDAVSVETQAYFNGTAYLPCPFTKAQNISLSELVVFWDQ 60
      MDP+CTMGL+ ++FV L+S A ++ QAYFN TA LPC F +QN SLSELVVFWDQ
Sbjct 1 MDPQCTMGLSNILFVMAFLLSGAAPLKIQAYFNETADLPCQFANSQNQSLSELVVFWDQ 60

Query 61 QKLVLVEHYLGTAKLDSVNAYLGRSFDNRNWTLLRLHNVQIKDMGSYDCFIQKKPPTGS 120
      + LVL E YLG EK DSV++KY+GRSFD ++WTLRLHN+QIKD G Y C I K PTG
Sbjct 61 ENLVLNEVYLGKEKFDVSHSKYMGRTSFDSDSWTLRLHNLQIKDKGLYQCIIHKKPTGM 120

Query 121 IILQQTLTELSVIANFSEPEIKLAQNVGTGNSGINLTCTSKQCHPKPKMYFLI--TNSTN 178
      I + Q +ELSV+ANFS+PEI N+T N INLTC+S G+P+PKKM L+ NST
Sbjct 121 IRIHQMNSELSVLANFSQPEIVPISNITENVYINLTCSSIHGYPEPKMSVLLRTKNSTI 180

Query 179 EYGDNMQISQDNVTelfsisnslslsfPDGVWHMTVVCVLETESMKISSKPLNFTQEFPS 238
      EY MQ SQDNVTEL+ +S SLS+SFPD +MT+ C+LET+ ++ S P + E P
Sbjct 181 EYDGVMQSQDNVTelydvsislsvsfpdvtsnmtifciletdktrllsppfsieleDPQ 240

Query 239 P---QTYWKEitasvtvalllvmllliivCHKKPNQPSRP----SNTASKLERDSNADRET 291
      P W + ++V LI+ KK +P +NT + E + RE
Sbjct 241 PPPDHPWITAVLPTVVICVMVFCLILWKKKKKRPNSYKCGTNTMERESEQTKKREK 300

Query 292 INLKE 296
      I++ E
Sbjct 301 IHIFE 305
```

CD28: 69%

>ref|NP_006130.1| CD28 antigen [Homo sapiens]
Length=220

GENE ID: 940 CD28 | CD28 molecule [Homo sapiens] (Over 100 PubMed links)

Score = 297 bits (760), Expect = 5e-81

Identities = 152/219 (69%), Positives = 171/219 (78%), Gaps = 5/219 (2%)

```
Query 3  LRLFLALNFF-SVQVTENKILVKQSPLLVVDSEVSLSCRYSYNLLAKEFRASLYKGVN 61
          LRL LALN F S+QVT NKILVKQSP+LV N V+LSC+YSYNL ++EFRASL+KG++
Sbjct 2  LRL-LALNLFPSIQVTGNKILVKQSPMLVAYDNAVNLSCKYSYNLFSREFRASLHKGLD 60

Query 62 SDVEVCVGNNGFTYQPQFRSNAEFNCDGDFDNETVTFRNLHVNHTDIYFCKIEFMYPP 121
          S VEVCV GN++ Q Q S FNC DG NE+VTF L NL+VN TDIYFCKIE MYPP
Sbjct 61 SAVEVCVVGNYSQLQVYSKTGFNCDGKLGNESVTFYLNLYVNQTDIYFCKIEVMYPP 120

Query 122 PYLDNERSNGTIIHIKEKHLCHTQSSP---KLFWLVVVAGVLFCYGLLVTVLVCVIWTN 178
          PYLDNE+SNGTIIH+K KHL C + P K FW LVVV GVL CY LLVTVA + W
Sbjct 121 PYLDNEKSGTIIHVKGKHLCPSPFPGPSKPFWWLVVVGVLACYSLLVTVAFIIFWVR 180

Query 179 SRRNRLLQSDYMNMTPRRPGLTRKPYQPYAPARDFAAAYR 217
          S+R+RLL SDYMNMTPRRPG TRK YQPYAP RDFAAAYR
Sbjct 181 SKRSRLLHSDYMNMTPRRPGPTRKHVQPYAPPRDFAAAYR 219
```

CD70: 56%

>ref|NP_001243.1| tumor necrosis factor ligand superfamily, member 7 [Homo sapiens]
Length=193

GENE ID: 970 CD70 | CD70 molecule [Homo sapiens] (Over 10 PubMed links)

Score = 195 bits (495), Expect = 2e-50

Identities = 110/195 (56%), Positives = 124/195 (63%), Gaps = 2/195 (1%)

```
Query 1  MPEEGRPCPWVRWSGTAFQRQWPWLLLVVFITVFCCWFHCSGLLSKQQQRLEHPEPHTA 60
          MPEEG C R R L+ +V V C QQQ LE A
Sbjct 1  MPEECGCSVRRRPYGCVLRAA--LVPLVAGLVICLVVCIQRFQAQQQLPLESLGWDVA 58

Query 61 ELQLNLTVPKRDPTLRWGAGPALGRSFTHGPELEEGLRIHQDGLYRLHIQVTLANCSSP 120
          ELQLN T P++DP L W GPALGRSF HGPEL++G LRIH+DG+Y +HIQVTLA CSS
Sbjct 59 ELQLNHTGPQQDPRLYWQGGPALGRSFLHGPELDKGQLRIHRDGIYMVHIQVTLAICSST 118

Query 121 GSTLQHRATLAVGICSPAAHGISLLRGRFGQDCTVALQRLTYLVHGDVLTNLTLPLLP 180
          ++ H TLAVGICSPA+ ISLLR F Q CT+A QRLT L GD LCTNLT LLPS
Sbjct 119 TASRHHPTTLAVGICSPASRSISLLRSLFHQGCCTIASQRLTPLARGDTLCTNLTGTLLPS 178

Query 181 RNADETFFGVQWICP 195
          RN DETFFGVQW+ P
Sbjct 179 RNTDETFFGVQWVRP 193
```

CD11b: 70%

>ref|NP_000623.2| integrin alpha M precursor [Homo sapiens]
Length=1152

GENE ID: 3684 ITGAM | integrin, alpha M (complement component 3 receptor 3 subunit) [Homo sapiens] (Over 100 PubMed links)

Score = 1765 bits (4571), Expect = 0.0

Identities = 863/1153 (74%), Positives = 1003/1153 (86%), Gaps = 1/1153 (0%)

Query	1	MtlkallvtalalCHGFNLDTEHPMTFQENAKGFGQSVVQLGGTSVVVAAPQEAKAVNQT	60
		M L+ LL+TAL LCHGFNLDTE+ MTFQENA+GFGQSVVQL G+ VVV APQE A NQ	
Sbjct	1	MALRVLLLTALTLCCHGFNLDTENAMTFQENARGFGQSVVQLQGSRVVVGAPQEIVAANQR	60
Query	61	GALYQCDYSTSRCHPIPLQVPPEAVNMSLGLSLAVSTVPQQLACGPTVHQNKENTYVN	120
		G+LYQCDYST C PI LQVP EAVNMSLGLSLA +T P QLLACGPTVHQ C ENTYY	
Sbjct	61	GSLYQCDYSTGSCPIRLQVPVEAVNMSLGLSLAATSPQQLACGPTVHQTCSENTYVK	120
Query	121	GLCYLFSGSNLLRPPQQFPEALRECPQESDIVFLIDSGSINNIDFQKMKEFVSTVMEQF	180
		GLC+LFSGSNL + PQ+FPEALR CPQ++SDI FLIDSGSI DF++MKEFVSTVMEQ	
Sbjct	121	GLCFLFGSNLRQQPQKFPEALRGCPQEDSDIAFLIDSGSIIIPHDFRRMKEFVSTVMEQL	180
Query	181	KKSKTLFSLMQYSDEFRIHFTFNDFKRNPSRSHVSPKQLNGRTKTASGIRKVVRELFH	240
		KKSKTLFSLMQYS+EFRIHFTF +F+ NP+PRS V PI QL GRT TA+GIRKVVRELF+	
Sbjct	181	KKSKTLFSLMQYSEEFRIHFTFKEFQNNPNPRSLVKPITQLLGRTHATGIRKVVRELFN	240
Query	241	KTNGARENAKILVVITDGEKFGDPLDYKDVIPEADRAGVIRYVIGVGNFNPQSRREL	300
		TNGAR+NA KILVVITDGEKFGDPL Y+DVIPEADR GVIRYVIGV+AF +SR+EL	
Sbjct	241	ITNGARKNAKILVVITDGEKFGDPLGYEDVIPEADREGVIRYVIGVDARSEKSRQEL	300
Query	301	DTIASKPAGEHVQVDNFEALNTIQNLQEKIFAIEGTQTGTSSTFEHMSQEGFSASIT	360
		+TIASKP +HVQV+NFEAL TIQNQL+EKIFAIEGTQTGS+SSFEHMSQEGFSA+IT	
Sbjct	301	NTIASKPPRDHVQVNNFEALKTIQNQLREKIFAIEGTQTGSSSSFEHMSQEGFSAAIT	360
Query	361	SNGPLLGSVGSFWDWAGGFLYTSKDKVTFINTTRVDSMDNDAYLGYASAVILNRNVQSLV	420
		SNGPLL +VGS+DWAGG FLYTSK+K TFIN TRVDSMDNDAYLGYA+A+ILNRNVQSLV	
Sbjct	361	SNGPLLSTVGSYDWAGGVFLYTSKEKSTFINMTRVDSMDNDAYLGYAAIILNRNVQSLV	420
Query	421	LGAPRYQHIGLVVMFRENFGTWEPHTSIKGSQIGSYFGASLCSVDMDADGNTNLILIGAP	480
		LGAPRYQHIGLV MFR+N G WE + ++KG+QIG+YFGASLCSVD+D++G+T+L+LIGAP	
Sbjct	421	LGAPRYQHIGLVAMFRQNTGMWESNANVKGTQIGAYFGASLCSVDVDSNGSTDLLVIGAP	480
Query	481	HYYEKTRGGQVSVCPPLPRGRARWQCEALLHGDQGHWPGRFGAALTVLGDVNGDKLTDVAI	540
		HYYE+TRGGQVSVCPPLPRGRARWQC+A+L+G+QG PWGRFGAALTVLGDVNGDKLTDVAI	
Sbjct	481	HYYEKTRGGQVSVCPPLPRGRARWQCDVLYGEQQGPWGRFGAALTVLGDVNGDKLTDVAI	540
Query	541	GAPGEQENQGAUVIFYGASIASLSASHSQRIIGAHSFPLQYFGQSLSGGKDLTMDGLMD	600
		GAPGE++N+GAVY+F+G S + +S SHSQRI G+ SP LQYFGQSLSGG+DLTMDGL+D	
Sbjct	541	GAPGEEDNRGAVYLFHGTSGSGISPSHSQRIAGSKLSPRLQYFGQSLSGGQDLTMDGLVD	600
Query	601	LAVGAQGHilllraqpvlriEATMEFSPKKVARSVFACQEQVLKNKDAGEVRVCLRVKRN	660
		L VQAQGH+LLLR+QPVL++A MEF+P++VAR+VF C +QV+K K+AGEVRVCL V+K+	
Sbjct	601	LTVGAQGHVLLRSQPVLRVKAIMFNPREVARNVFECNDQVVKGEAGEVRVCLHVQKS	660

Query	661	TKDRLREGDIQSTVTYDLALDPGRSRIRAFFDETKNNTRRRRTQVFGLMQKCETLKLILPD	720
		T+DRLREG IQS VTYDLALD GR RA F+ETKN+TRR+TQV GL Q CETLKL LP+	
Sbjct	661	TRDRLREGQIQSVVTYDLALDSGRPHSRAVFNETKNSTRRQTQVGLTQTCETLKLQLPN	720
Query	721	CVDDSVSPIIILRLNYTLVGEPLRSFGNLRPVLAMDAQRFFTAMFPFEKNCGNDSICQDDL	780
		C++D VSPI+LRLN++LVG PL +FGNLRPVLA DAQR FTA+FPFEKNCGN+ICQDDL	
Sbjct	721	CIEDPVSPIVLRLNFSLVGTPLSAFGNLRPVLAEDAQRLFTALFPFEKNCGN+ICQDDL	780
Query	781	SITMSAMGLDTLVVGGPQDFNMSVTLRNDGEDSYGTQVTVYYPSGLSYRKDSASQNPLTK	840
		SIT S M LD LVVGGP++FN++VT+RNDGEDSY TQVT ++P LSYRK S QN ++	
Sbjct	781	SITFSMSLDCLLVGGPREFNVTVTVRNDGEDSYRTQVTFFFLDLSYRKVSTLQNRSQ	840
Query	841	KPWFVKPAessssseGHGALKSTTWNINHPIFPANSEVTFNVTDFVDSHASFGNKLLKA	900
		+ W + ES+SS+E GALKST+ +INHPIFP NSEVTFN+TFDVDS AS GNKLLKA	
Sbjct	841	RSWRL-ACESASSTEVSGALKSTSCSINHPIFPENSEVTFNITFDVDSKASLGNKLLKA	899
Query	901	IVASENNMSRTHKTKFQLELPVKYAIYMIVTSDESSIRYLNFTASEMTSKVIQHQQFNN	960
		V SENNM RT+KT+FQLELPVKYA+YM+VTS S +YLNFTASE TS+V+QHQQ +N	
Sbjct	900	NVTSENNMPRTNKTEFQLELPVKYAVYMVVTSHGVS TKYLNFTASENSTRVMQHQQVSN	959
Query	961	LGQRSLPVSVFWIPVQINNVTVDHPQVIFSQNLSSACHTEQKSPPHSNFRDQLERTPV	1020
		LGQRSLP+S+VF +PV++N +WD PQV FS+NLSS CHT+++ P HS+F +L + PV	
Sbjct	960	LGQRSLPISLVFLVPVRLNQTVIWRPQVTFSENLSSTCHTKERLPSHSDFLAELRKAPV	1019
Query	1021	LNCSYAVCKRIQCDLPSFNTQEIFNVTLKGNLSFDWYIKTSHGHLLLVSSTEILFNDSAF	1080
		+NCS+AVC+RIQCD+P F QE FN TLKGNLSFDWYIKTSH HLL+VS+ EILFNDS F	
Sbjct	1020	VNCSIAVCQRIQCDIPFFGIQEEFNATLKGNLSFDWYIKTSHNLLIVSTAELFNDSVF	1079
Query	1081	ALLPGQESYVRSKTETKVEPYEVHNPVPLIVGSSIGGLVLLALITAGLYKLGFQKQYKD	1140
		LLPGQ ++VRS+TETKVEP+EV NP+PLIVGSS+GGL+LLALITA LYKLGFQKQYKD	
Sbjct	1080	TLLPGQGAFVRSQTETKVEPFEVNPPLPLIVGSSVGLLLALITAALYKLGFQKQYKD	1139
Query	1141	MMNEAAPQDAPPQ	1153
		MM+E P A PQ	
Sbjct	1140	MMSEGGPPGAEPQ	1152

CD18: 81%

>ref|NP_000202.2| integrin, beta 2 precursor [Homo sapiens]
Length=769

GENE ID: 3689 ITGB2 | integrin, beta 2 (complement component 3 receptor 3 and 4 subunit) [Homo sapiens] (Over 100 PubMed links)

Score = 1351 bits (3497), Expect = 0.0

Identities = 632/771 (81%), Positives = 694/771 (90%), Gaps = 2/771 (0%)

```
Query 1  MlglrpslllalaglfflgsaVSQECTKYKVSSCRDCIQSGPGCSWCQKLNFTGPGEPS 60
          MLGLRP LL AL GL LG +SQECTK+KVSSCR+CI+SGPGC+WCQKLNFTGPG+PDS
Sbjct 1  MLGLRPPLL-ALVGLLSLGCVLSQECTKFKVSSCRECIESGPGCTWCQKLNFTGPGDPDS 59

Query 61  LRCDTRAQLLLKCPADDIMDPRSIANPEFDQRGQRKQLSPQKVTLYLPGQAAAFNVTF 120
          +RCDTR QLL++GC ADDIMDP S+A + D G +KQLSPQKVTLYLPGQAAAFNVTF
Sbjct 60  IRCDTRPQLLMRGCAADDIMDPTSLAETQEDHNGGQKQLSPQKVTLYLPGQAAAFNVTF 119

Query 121  RRAKGYPIdlylmdlsysmlddINNKKLGGDLLQALNEITESGRIGFGSFVDKTVLPF 180
          RRAKGYPIDLYYLMDSLYSMLDDL NVKKLGGDLL+ALNEITESGRIGFGSFVDKTVLPF
Sbjct 120  RRAKGYPIDLYYLMDSLYSMLDDLNRVKKLGGDLLRALNEITESGRIGFGSFVDKTVLPF 179

Query 181  VNTHPEKLRNPCPNKEKACQPPFAFRHVLKLTDNSNQFQTEVGKQLISGNLDAPEGGLDA 240
          VNTHP+KL RNPCPNKEK CQPPFAFRHVLKLT+NSNQFQTEVGKQLISGNLDAPEGGLDA
Sbjct 180  VNTHPKLRNPCPNKEKECQPPFAFRHVLKLTNNSNQFQTEVGKQLISGNLDAPEGGLDA 239

Query 241  IMQVAACP E EIGWRNVTRLLVFATDDGFHFAGDGKLGAILTPNDGRCHLEDNMYKRSNEF 300
          +MQVAACP E EIGWRNVTRLLVFATDDGFHFAGDGKLGAILTPNDGRCHLEDN+YKRSNEF
Sbjct 240  MMQVAACP E EIGWRNVTRLLVFATDDGFHFAGDGKLGAILTPNDGRCHLEDNLYKRSNEF 299

Query 301  DYPSVGQLAHKLSESNIQPIFAVTKKMVKTYEKLTEIIPKSAVGELSDDSSNVVQLIKNA 360
          DYPSVGQLAHKL+E+NIQPIFAVT +MVKTYEKLTEIIPKSAVGELS+DSSNVVQLIKNA
Sbjct 300  DYPSVGQLAHKLAENNIQPIFAVTSRMVKTYEKLTEIIPKSAVGELSEDSSNVVQLIKNA 359

Query 361  YYKLSSRVFLDHSTLPDTLKVTYDSFCSNGASSIGKSRGDCDGVQINNPVTFQVKVMASE 420
          Y KLSSRVFLDH+ LPDTLKVTYDSFCSNG + + RGDCDGVQIN P+TFQVKV A+E
Sbjct 360  YNKLSSRVFLDHNALPDTLKVTYDSFCSNGVTHRNQPRGDCDGVQINVPITFQVKVTATE 419

Query 421  CIQE QSFVIRALGFTDVTVQVRPQCECQCRDQSRQSLCGGKGVMECGICRCESGYIGK 480
          CIQE QSFVIRALGFTD VTVQV PQCEC+CRDQSR++SLC GK +ECGICRC++GYIGK
Sbjct 420  CIQE QSFVIRALGFTDIVTVQVLPQCECQCRDQSRDRSLCHGKGFLECGICRCDTGYIGK 479

Query 481  NCECQTQGRSSQELERNCRKDNSSIIVCSGLGDCICGQCVCHTSDVPNKEIFGQYCECDNV 540
          NCECQTQGRSSQELE +CRKDN+SI+CSGLGDC+CGQC+CHTSDVP K I+GQYCECD +
Sbjct 480  NCECQTQGRSSQELEGSCRKDNNSIICSGLGDCVCGQCLCHTSDVPKLIYGQYCECDTI 539

Query 541  NCERYNSQVCGGSDRGSCNCGKCSCKPGYEGSACQCQRSTTGCLNARLVECSGRGHCQCN 600
          NCERYN QVCGG RG C CGKC C PG+EGSACQC+R+T GCLN R VECSSRG C+CN
Sbjct 540  NCERYNQVCGGPGRGLCFCKCRCHPGFECSACQCERTTEGCLNPRRVECSGRGRCRCN 599

Query 601  RCICDEGYQPPMCEDPCSGSHCRDNHTSCAECLKFKDKPFKNCQSVQCAGMTLQTIPLK 660
          C C GYQ P+C++CP C S C + SCAECLKF+KGP KNC C G+ L P+K
Sbjct 600  VCECHSGYQLPLCQECPCGSPC-GKYISCAECLKFEKGPFGKNC SAACPGLQLSNNPVK 658
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Query 661 KKPCKERDSEGCWITYTLQQKDGRNIYNIHVEDSLECVKGPNVAAIvggtvvvgvligvl 720
+ CKERDSEGCW+ YTL+Q+DG + Y I+V++S ECV GPN+AAIVGGTV G+VLIG+L
Sbjct 659 GRTCKERDSEGCWVAYTLEQQDGMdryLIYVDESRECVAGPNIAAIVGGTVAGIVLIGIL 718

Query 721 llviWKALThLTDLREYRRFEKEKLKSQWNNDNPLFKSATTVMNPKFAES 771
LLVIWKAL HL+DLREYRRFEKEKLKSQWNNDNPLFKSATTVMNPKFAES
Sbjct 719 LLVIWKALIHLSDLREYRRFEKEKLKSQWNNDNPLFKSATTVMNPKFAES 769

CD23: 54%

>ref|NP_001993.2| Fc fragment of IgE, low affinity II, receptor for (CD23A) [Homo sapiens]
Length=321

GENE ID: 2208 FCER2 | Fc fragment of IgE, low affinity II, receptor for (CD23)
[Homo sapiens] (Over 10 PubMed links)

Score = 373 bits (957), Expect = 1e-103

Identities = 179/331 (54%), Positives = 236/331 (71%), Gaps = 23/331 (6%)

```
Query 1  MEENEYSGYWEPKRKRCCARRGTQLMLVGLLSTAMWAG11a1111WHWETEKNLKQLGD 60
      MEE +YS  E PR+RCC  RRGTQ++L+GL++ A+WAGLL LLLLWHW+T ++LKQL +
Sbjct 1  MEEGQYSEIEELPRRRCC--RRGTQIVLLGLVTAALWAGLLTLLLWHWDTTQSLKQLEE 58

Query 61  TAIQNVSHVTKDLQKFQSNQLAQKSQVVQMSQNLQELQAEQKQMKQAQDSRLSQNLTLGLQE 120
      A +NVS V+K+L+  +Q+AQKSQ  Q+SQ L+EL+AEQ+++K+QD  LS NL G
Sbjct 59  RAARNVSQVSKNLESHHGDAQMAQKSQSTQISQELEELRAEQRLKSQDLELSWNLNG--- 115

Query 121  DLRNAQSQNSKLSQNLNRLQDDLVDNIKSLGLNEKRTASDSLEKLQEEVAKLWIEILISKG 180
      LQ DL + KS  LNE+  ASD LE+L+EEV KL +E+ +S G
Sbjct 116  -----LQADLSSFKSQELNERNEASDLLERLREEVTKLRMELQVSSG 157

Query 181  TACNICPKNLWHFQQKCYFYGKGSQWIIQARFACSDLQGRVLSIHSQKEQDFLMQHINKK 240
      CN CP+ W+++FQ+KCYFYGKG+KQW+ AR+AC D++G+LVSIS +EQDFL +H +
Sbjct 158  FVCNTCPEKWINFQRKCYFYGKGTKQVWHARYACDDMEGQLVSIHSPEEQDFLTKHASHT 217

Query 241  DSWIGLQDLNMEGEFVWSDGSPVGYSnwnpgepnnggqgeDCVMMRGSGQWDAFCRSYL 300
      SWIGL++L+++GEF+W DGS V YSNW PGEP + QGEDCVMMRGSG+WDAFC  L
Sbjct 218  GSWIGLRNLDLKGEFIWVDGSHVDYSNWAPGEPTSRSQGEDCVMMRGSGRWDAFCDRKL 277

Query 301  DAWVCEQLATCEISAPLASVTPTPTPKSEP 331
      AWVC++LATC  A  S  P  + +P
Sbjct 278  GAWVCDRLATCTPPASEGSAESMGPDSPDP 308
```

ICAM-1: 53%

>ref[NP_000192.1] intercellular adhesion molecule 1 precursor [Homo sapiens]
Length=532

GENE ID: 3383 ICAM1 | intercellular adhesion molecule 1 (CD54), human
rhinovirus receptor [Homo sapiens] (Over 100 PubMed links)

Score = 525 bits (1352), Expect = 4e-149

Identities = 287/540 (53%), Positives = 363/540 (67%), Gaps = 11/540 (2%)

```
Query 1  MASTRAKptlplllalvtvvIPGPGDAQVSIHPREAFLPQGGSVQVNCSSSCKEDLSLGL 60
      MA + +P LP LL L+ + PGP+AQ S+ P + LP+GGSV V CS+SC + LG+
Sbjct 1  MAPSSPRPALPALLVLLGALFPGPGNAQTSVSPSKVILPRGGSVLVTCSTSCDQPKLLGI 60

Query 61  ETQWLKDELE-SGPNWKLFESEIGEDSSPLCFENC GTVQSSASATITVVSFPESVELRP 119
      ET K EL G N K++ELS + EDS P+C+ NC QS+A +TVY PE VEL P
Sbjct 61  ETPLPKKELLPLGNRKVYELSNVQEDSQPMCSNCPDQGSTAKTFLTIVYWTPERVELAP 120

Query 120  LPAWQQVGKDLTLRCHVDGGAPRTQLSAVLLRGEEILSRQPVGGHPKPKKEITFTVLASR 179
      LP+WQ VGK+LTLRC V+GGAPR L+ VLLRGE+ L R+P G +P E+T TVL R
Sbjct 121  LPSWQPVGKNLTLRCQVEGGAPRANLTVVLLRGEKELKREPAVG---EPAEVTTTVLVR 177

Query 180  GDHGANFSCRTDLRLPQGLALFSNVSEARSLRTFDLPATIPKLDTPDLLEVGTQQKLCFC 239
      HGANFSCRTDLRLPQGL LF N S L+TF LPAT P+L +P +LEV TQ + C
Sbjct 178  DHGANFSCRTDLRLPQGLELFENTSAPYQLQTFLPATPPQLVSPRVLEVDTQGTVC 237

Query 240  SLEGLFPASEARIYLELGGQMPTQESTNSSDSVSATALVEVTEEFDRTLPLRCVLELADQ 299
      SL+GLFP SEA+++L LG Q T +DS SA A V VT E + T L C + L +Q
Sbjct 238  SLDGLFPVSEAEQVHLALGDQRLNPTVTYGNDSFSAKASVSVTADEGTQRLTCAVILGNQ 297

Query 300  ILETQRTLTVYNFSAPVLTLSQLEVSEGSQVTVKCEAHSGSKVLLSGVEPRPPTPQVQF 359
      ET +T+T+Y+F AP + L++ EVSEG++VTVKCEAH +KV L+GV +P P+ Q
Sbjct 298  SQETLQTVTIYSFPAPNVILTKPEVSEGTEVTVKCEAHPRAKVT-LNGVPAQPLGPRAQL 356

Query 360  TLNASEDHKRSFFCSAALEVAGKFLFKNQTLHLVLYGPRLDETDCLGNTWQEGSQQT 419
      L A+ ED+ RSF CSA LEVAG+ + KNQT EL VLYGPRLDE DC GNWTW E SQQT
Sbjct 357  LLKATPEDNGRSFSCSATLEVAGQLIHKNTRELRLVLYGPRLDERDCPGNWTWPENSQQT 416

Query 420  LKCQAWGNPSPKMTCCRKADGAL-LPIGVVKSVMQEMNGTYVCHAFSSHGNVTRNVYLT 478
      CQAWGNP P++ C + DG LPIG +V +++ GTY+C A S+ G VTR V + V
Sbjct 417  PMCQAWGNPLPELCLK--DGTFLPIGESVTVTRDLEGTLYLCRARSTQGEVTREVTNV 474

Query 479  LYHSQNNWTiilvpvllvivglvMAASYVYNRQRKIRIYKLQKAQE-EAIKLKGQAPPP 537
      L S +II V VI+G ++Y+YNRQRKI+ Y+LQ+AQ+ +K QA PP
Sbjct 475  L--SPRYEIVIIITVVAADVIMGTAGLSTYLYNRQRKIKKYRLQQAQKGTMPKPNTQATPP 532
```

VLA-4 Integrin Receptor: 84%

>ref|NP_000876.3| integrin alpha 4 precursor [Homo sapiens]
Length=1032

GENE ID: 3676 ITGA4 | integrin, alpha 4 (antigen CD49D, alpha 4 subunit of VLA-4 receptor) [Homo sapiens] (Over 10 PubMed links)

Score = 1790 bits (4636), Expect = 0.0

Identities = 871/1025 (84%), Positives = 951/1025 (92%), Gaps = 0/1025 (0%)

Query	15	DQGPRGIALREAVMLLLYFGVPTGPSYNLDPENALLYQGPGSTLFGYSVVLHSHGSKRWL	74
		+ GPR A+RE VMLLL GVPTG YN+D E+ALLYQGP TLFGYSVVLHSHG+ RWL	
Sbjct	8	EPGPRRAAVRETVMLLCLGVPTGRPYNVDTESALLYQGPHTLFGYSVVLHSHGANRWL	67
Query	75	IVGAPTASWLSNASVVPNGAIYRCGIRKNPNQTCEQLQSGSPSGEPCGKTCLEERDNQWL	134
		+VGAPTA+WL+NASV+NPNGAIYRC I KNP QTCEQLQ GSP+GEPGKTCLEERDNQWL	
Sbjct	68	LVGAPTANWLANASVINPGAIYRCRIGNPGQTCEQLQLGSPNGEPCGKTCLEERDNQWL	127
Query	135	GVTLSRQPGENGSIIVTCGHRWKNIFYMKSDNKLPTGICYVMPSDLRTELSKRMAPCYKDY	194
		GVTLSRQPGENGSIIVTCGHRWKNIFY+K++NKLPTG CY +P DLRTLSKR+APCY+DY	
Sbjct	128	GVTLSRQPGENGSIIVTCGHRWKNIFYIKNENKLPTGGCYGVPPDLRTELSKRIPACYQDY	187
Query	195	TRKFGENFASCQAGISSFYTDLIVMGAPGSSYWTGTVFVYNITTNQYKAFVDRQNQVKF	254
		+KFGENFASCQAGISSFYT+DLIVMGAPGSSYWTG++FVYNITTN+YKAF+D+QNQVKF	
Sbjct	188	VKKFGENFASCQAGISSFYTKDLIVMGAPGSSYWTGSLFVYNITTNKYKAFLDKQNQVKF	247
Query	255	GSYLGYSYGAGHFRSPHTTEVVGGAPQHEQIGKAYIFSIDENELNIVYEMKGKGLGSYFG	314
		GSYLGYSYGAGHFRS HTTEVVGGAPQHEQIGKAYIFSIDE ELNI++EMKGKGLGSYFG	
Sbjct	248	GSYLGYSYGAGHFRSQHTTEVVGGAPQHEQIGKAYIFSIDEKELNILEMKGKGLGSYFG	307
Query	315	ASVCAVDLNADGFSDDL VGAPMQSTIREGRVFVYINSGMGAVMVERVLVGS DKYAAR	374
		ASVCAVDLNADGFSDDL VGAPMQSTIREGRVFVYINSG GAVM ME LVGS DKYAAR	
Sbjct	308	ASVCAVDLNADGFSDDL VGAPMQSTIREGRVFVYINSGSGAVMNAMETNLVGS DKYAAR	367
Query	375	FGESIANLGDIDNDGFEDIAIGAPQEDDLRGAVYIYNGRVDGISSTYSQRIEQQISKSL	434
		FGESI NLGDIDNDGFED+AIGAPQEDDL+GA+YIYNGR DGISST+SQRIEQ QISKSL	
Sbjct	368	FGESIVNLGDIDNDGFEDVAIGAPQEDDLQGAIIYNGRADGISSTFSQRIEGLQISKSL	427
Query	435	RMFGQSISGQIDADNNGYVDVAVGAFQSDSAVLLRTRPVVIVEASLSHPESVNRTKFDC	494
		MFGQSISGQIDADNNGYVDVAVGAF+SDSAVLLRTRPVVIV+ASLSHPESVNRTKFDC	
Sbjct	428	SMFGQSISGQIDADNNGYVDVAVGAFRSDSAVLLRTRPVVIDASLSHPESVNRTKFDCV	487
Query	495	ENGLPSVCMHLTLCSYKGKEVPGYIVLFYNVSLDVHRKAESPSRFYFFSNGTSDVITGS	554
		ENG PSVC+ LTLCSYKGKEVPGYIVLFYN+SLDV+RKAESP RFYF SNGTSDVITGS	
Sbjct	488	ENGWPSVCIDLTLCSYKGKEVPGYIVLFYNMSLDVNRKAESPFRFYFSSNGTSDVITGS	547
Query	555	IRVSSSGEKRTHQAFMRKDVRDILTPIHVEATYHLGHHVITKRNTTEFPPLQPILOQKK	614
		I+VSS CRTHQAFMRKDVRDILTPI +EA YHLG HVI+KR+TEFPPLQPILOQKK	
Sbjct	548	IQVSSREANCRTHQAFMRKDVRDILTPIQIEAAYHLGPHVISKRSTEEFPPLQPILOQKK	607
Query	615	EKDVIKMINFARFCAYENCADLQVSAKVGFLKPYENKTYLAVGSMKTMNLNVSLFNAG	674
		EKD+++K INFARFCA+ENCADLQVSAK+GFLKP+ENKTYLAVGSMKT+MLNVSLFNAG	
Sbjct	608	EKDIMKKTINFARFCAHENCADLQVSAKIGFLKPHENKTYLAVGSMKTMNLNVSLFNAG	667

Query	675	DDAYETTLNVQLPTGLYFIKILDLEEKQINCEVTESSGIVKLACSLGYIYVDRLSRIDIS	734
		DDAYETTL+V+LP GLYFIKIL+LEEKQINCEVT++SG+V+L CS+GYIYVD LSRIDIS	
Sbjct	668	DDAYETTLHVKLPPVGLYFIKILELEEKQINCEVTDNSGVVQLDCSIGIYVDHLSRIDIS	727
Query	735	FLLDVSSLSRAHEDLSISVHASCENEGELDQVRDNRVTLTIPLRYEVM LTVHGLVNPTSF	794
		FLLDVSSLSRA EDLSI+VHA+CENE E+D ++ +RVT+ IPL+YEV LTVHG VNPTSF	
Sbjct	728	FLLDVSSLSRAEEDLSITVHATCENEEEMDNLKHSRVTVAIPLKYEK LTVHGFVNPTSF	787
Query	795	VYGSSEENEPETCMAEKLNLTFHVINTGISMAPNVSVKIMVPNSFLPQDDKLFNVDVQT	854
		VYGS++ENEPETCM EK+NLTFHVINTG SMAPNVSV+IMVPNSF PQ DKLFN+LDVQT	
Sbjct	788	VYGSNDENEPETCMVEKMNLTFHVINTGNSMAPNVSV+IMVPNSFSPQTDKLFNILDVQT	847
Query	855	TTGQCHFKHYGRECTFAQQKGIAGTLTDIVKFLSKTDKRLLYCMKADQHCLDFLCNFGKM	914
		TTG+CHF++Y R C QQK TL IV+FLSKTDKRLLYC+KAD HCL+FLCNFGKM	
Sbjct	848	TTGECHFENYQRVCALEQQKSAMQTLKGIVRFLSKTDKRLLYCIKADPHCLNFCNFGKM	907
Query	915	ESGKEASVHIQLEGRPSILEMDETSSLKFEIKATAFPEPHPKVIELNKDENVAHVLEGL	974
		ESGKEASVHIQLEGRPSILEMDETS+LKFEI+AT FPEP+P+VIELNKDENVAHV LEGL	
Sbjct	908	ESGKEASVHIQLEGRPSILEMDETSALKFEIRATGFPEPNRVIELNKDENVAHVLEGL	967
Query	975	HHQRPKRHFTiiiiitislilglivllliSCVMWKAGFFKRQYKSILQEENRRDSWSYVNS	1034
		HHQRPKR+FTI+II+ SLLGLIVLLLIIS VMWKAGFFKRQYKSILQEENRRDSWSY+NS	
Sbjct	968	HHQRPKRYFTIIVIISSSLLGLIVLLLIISYVMWKAGFFKRQYKSILQEENRRDSWSYINS	1027
Query	1035	KSND	1039
		KSND	
Sbjct	1028	KSND	1032

IL-1 β Receptor: 62%

>ref|NP_004624.1| interleukin 1 receptor, type II precursor [Homo sapiens]
ref|NP_775465.1| interleukin 1 receptor, type II precursor [Homo sapiens]
Length=398

GENE ID: 7850 IL1R2 | interleukin 1 receptor, type II [Homo sapiens]
(Over 10 PubMed links)

Score = 474 bits (1220), Expect = 5e-134
Identities = 231/371 (62%), Positives = 280/371 (75%), Gaps = 2/371 (0%)

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Query 28  NCQFRGREFKSELRLGEGPVVLRCLAPHdisssshsF-LTWSKLDSSQLIP-RDEPRM 85
          +C+FRGR +K E RLECEPV LRCP P+ +S S   LTW K DS++ +P +E RM
Sbjct 27  SCRFRGRHYKREFRLEGEVALRCPQVPYWLWASVSPRINLTWHKNSARTVPGEETR 86

Query 86  WVKGNILWILPAVQQDSGTYICTFRNASHCEQMSVELKVFKNTEASLPHVSYLQISALST 145
          W +   LW+LPA+Q+DSGTY+CT RNAS+C++MS+EL+VF+NT+A LP +SY QI  LST
Sbjct 87  WAQDGALWLLPALQEDSGTYVCTTRNASYCDKMSIELRVFENTDAFLPFISYPQILTST 146

Query 146 TGLLVCPDLKEFISSNADGKIQWYKGAILLDKGNKEFLSAGDPTRLLISNTSMDDAGYYR 205
          +G+LVCPDL EF   D KIQWYK ++LLDK N++FLS   T LL+ + +++DAGYYR
Sbjct 147 SGVLVCPDLSEFTRDKTDVKIQWYKDSLLLDKDNKEFLSVRGTTLLVHDVALEDAGYYR 206

Query 206 CVMFTFYNGQEYNITRNIELRVKGTTEPIPVIIISPLETIPASLGSRLIVPCKVFLGTGT 265
          CV+TF + GQ+YNITR+IELR+K   E IPVIIISPL+TI ASLGSRL +PCKVFLGTGT
Sbjct 207 CVLTFHEGQQYNITRSIELRIKKKKEETIPVIIISPLKTISASLGSRLTIPCKVFLGTGT 266

Query 266 SSNTIVWWLANSTFISAAYPRGRVTEGLHHQYSENDENYEVSLIFDPVTREDLHTDFKC 325
          T++WW AN T I +AYP GRVTEG   +YSEN+ENY+EV LIFDPVTREDLH DFKC
Sbjct 267 PLTTMLWWTANDTHIESAYPGGRVTEGPRQEYSENNENYIEVPLIFDPVTREDLHMDFKC 326

Query 326 VASNPRSSQSLHTTVKEVSSTFSW$ialaplsliilVVGAIWMRRRCKRRAGKTYGLTKL 385
          V N S Q+L TTVKE SSTFSW I LAPLSL LV+G IWM RRCK R GK GLT L
Sbjct 327 VVHNTLSFQTLRTTVKEASSTFSWGIVLAPLSLAFLVLGGIWMHRRCKHRTGKADGLTVL 386

Query 386 RTDNQDFPSSP 396
          +QDF S P
Sbjct 387 WPHHQDFQSYP 397
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GPIIb: 79%

>ref|NP_000410.2| integrin alpha 2b preproprotein [Homo sapiens]

Length=1039

GENE ID: 3674 ITGA2B | integrin, alpha 2b (platelet glycoprotein IIb of IIb/IIIa complex, antigen CD41) [Homo sapiens] (Over 100 PubMed links)

Score = 1681 bits (4354), Expect = 0.0

Identities = 831/1040 (79%), Positives = 910/1040 (87%), Gaps = 11/1040 (1%)

Query	1	MARASCAWHSLWLLQWTPFLGPSAVPPVWALNLDSEKFSVYAGPNGSHFGFSVDFHKDK	60
		MARA C +LWLL+W L LCP A PP WALNLD + + YAGPNGS FGFS+DFHKD	
Sbjct	1	MARALCPLQALWLEWVLLLLGPCAAPPWALNLDPVQLTFYAGPNGSQFGFSLDFHKDS	60
Query	61	HGSVSIVVGAPRALNASQEETGAVFLCPWKANGGKCNPLLFDLRDETRNLGFQIFQTFKT	120
		HG V+IVVGAPR L SQEETG VFLCPW+A GG+C LLFDLRDETRN+G Q QTFK	
Sbjct	61	HGRVAIVVGAPRTLGPSQEETGGVFLCPWRAEGGQCPSELLFDLRDETRNVGSQTLQTFKA	120
Query	121	GQGLGASVVSWN DIVACAPWQHWNVLEKRDEAEKTPVGGCFLAQLQSGGRAEYSPCRAN	180
		QGLGASVVS+W DIVACAPWQHWNVLEK +EAEKTPVG CFLAQ +SG RAEYSPCR N	
Sbjct	121	RQGLGASVVS+SDVIVACAPWQHWNVLEKTEEAETPVGSCFLAQPESGRRAEYSPCRGN	180
Query	181	TMSSVYAES-FRGDKRYCEAGFSLAVTQAGELVLGAPGGYFFLGLLARVPIENIISTYRP	239
		T+S +Y E+ F DKRYCEAGFS VTQAGELVLGAPGGY+FLGLLA+ P+ +I S+YRP	
Sbjct	181	TLSRIYVENDFSWDKRYCEAGFSSVVTQAGELVLGAPGGYFFLGLLAQAPVADIFSSYRP	240
Query	240	GTLWHVSNQRFTYDNSNPVFFDGYRGYSVSVGEFDGDPSTTEYVSGAPTWSWTLGAVEI	299
		G LLWHVS+Q ++D+SNP +FDGY GYSV+VGEFDGD +TTEYV GAPTWSWTLGAVEI	
Sbjct	241	GILLWHVSSQSLSFDSNPPEYFDGYWGYSVAVGEFDGDLNTEYVVGAPTWSWTLGAVEI	300
Query	300	LDSYYQLHRLHGEQMASYFGHSVAVTDVNGDGRHDL LVGAPLYMESRADRKLAEVGRVY	359
		LDSYYQ LHRL GEQMASYFGHSVAVTDVNGDGRHDL LVGAPLYMESRADRKLAEVGRVY	
Sbjct	301	LDSYYQLHRLRGEQMASYFGHSVAVTDVNGDGRHDL LVGAPLYMESRADRKLAEVGRVY	360
Query	360	LFLQPKGPALSTPTLLLTGTQLYGRFGSAIAPLGDLNRDGYNDIAVAAPYGGPSGQGV	419
		LFLQP+GP AL P+LLLTGTQLYGRFGSAIAPLGDL+RDGYNDIAVAAPYGGPSG+GQV	
Sbjct	361	LFLQPRGPHALGAPSLLLTGTQLYGRFGSAIAPLGDLDRDGYNDIAVAAPYGGPSGRGQV	420
Query	420	LIFLGQSEGLSPRPSQVLDSPFPTGSGFGFSLRGAVDIDDNGYPDLIVGAYWASKVAVYR	479
		L+FLGQSEGL RPSQVLDSPFPTGS FGFSLRGAVDIDDNGYPDLIVGAY A++VAVYR	
Sbjct	421	LVFLGQSEGLSRPSQVLDSPFPTGSFSGFSLRGAVDIDDNGYPDLIVGAYGANQVAVYR	480
Query	480	AQPGVMATVQLMVQDSLNP TLKNCVLDQTKTPVSCFNIQMCVGATGHNIPQKLHLKAEQ	539
		AQP V A+VQL+VQDSLNP +K+CVL QTKTPVSCFNIQMCVGATGHNIPQKL L AELQ	
Sbjct	481	AQPVVKASVQLLVQDSLNPVAVKSCVLPQTKTPVSCFNIQMCVGATGHNIPQKLSLNAELQ	540
Query	540	LDLQKPRQRRVlllasqqasltlsldlGGRDKPICHHTGAFLRDEADFRDKLSPIVLSL	599
		LD QKPRQRRVLLL SQA TL+LDLGG+ PICHHT AFLRDEADFRDKLSPIVLSL	
Sbjct	541	LDRQKPRQRRVLLLSQAAGTTLNLDLGGKHPICHHTMAFLRDEADFRDKLSPIVLSL	600
Query	600	NVSLPPEETGGAPAVVLHGETHVQEQTRIILDCGEDDLCPQLRLTATAGDSPLLIGADN	659
		NVSLPP E G APAVVLHG+THVQEQTRI+LDCGEDD+CPVQL+LTA+ SPL+GADN	
Sbjct	601	NVSLPPEAGMAPAVVLHGDTHVQEQTRIVLDCGEDDVCVPQLQLTASVTGSPLLIGADN	660

Query	660	VLELKIEAANDGEGAYEAE LAVHLP GAHYMRALS NIEGFERLVCTQKKENESRVALCEL	719
		VLEL+++AAN+GEGAYEAE LAVHLP GAHYMRALS N+EGFERL+C QKKENE+RV LCEL	
Sbjct	661	VLELQMDAANE GEGAYEAE LAVHLPQGAHYMRALS NVEGFERLICNQKKENETRVLCEL	720
Query	720	GNPMKKDTRIGITMLVSVENLEEAGESVSFQLQVRSKNSQNPNSKVVMLPVAIQAEATVE	779
		GNPMKK+ +IGI MLVSV NLEEAGESVSFQLQ+RSKNSQNPNSK+V+L V ++AEA VE	
Sbjct	721	GNPMKNAQIGIAMLVSVGNLEEAGESVSFQLQIRSKNSQNPNSKIVLLDVPVRAEAQVE	780
Query	780	LRGNSFPASLVVAAEEGDREQEDLDSWVSRLHTYELHNIGPCTVNGLRLLIHIPGQSQP	839
		LRGNSFPASLVVAAEEG+REQ LDSW ++EHTYELHN GPCTVNGL L IH+PGQSQP	
Sbjct	781	LRGNSFPASLVVAAEEGEREQNSLDSWGPKEHTYELHNNGPCTVNGLHLSIHLPGQSQP	840
Query	840	SDLLYILDVQPQGGLLCSTQPSP---KVDWKLSTPSPSSIRPVHHQRERRQAFLQGPKPG	896
		SDLLYILD+QPQGGL C QP KVDW L PSPS I P HH+R+RRQ FL P+P	
Sbjct	841	SDLLYILDIQPQGGLQCFPPPVNPLKVDWGLPIPSPSPIHPAHHKDRRQIFL--PEPE	898
Query	897	Q---QDPVLVSCDGSASCTVVECELREMVRCGRAMVTVQAMLGLSSLRQRPQEQFVLQS	952
		Q QDPVLVSCD SA CTVV+C+L+EM RGGRAMVTV A L L SL QRP +QFVLQS	
Sbjct	899	QPSRLQDPVLVSCD-SAPCTVVQCDLQEMARGGRAMVTVLAFLWLP SLYQRPLDQFVLQS	957
Query	953	HAWFNvsslpsvpsvslpsGQARVQTQLLRALEERAIPVWVlvglgglllltllv1A	1012
		HAWFNVSSLPY+VP +SLP G+A+V TQLLRALEERAIP+WWVLGVLGGLLLLT+LVLA	
Sbjct	958	HAWFNVSSLPYAVPPLSLPRGEAQVWTQLLRALEERAIPiWWVLGVLGGLLLLTILVLA	1017
Query	1013	MWKAGFFKRNRPLEEDEEE	1032
		MWK GFFKRNRPLEED+EE	
Sbjct	1018	MWKGFFKRNRPLEEDEE	1037

GPIIb Receptor: 90%

>ref|NP_000203.2| integrin beta chain, beta 3 precursor [Homo sapiens]
Length=788

GENE ID: 3690 ITGB3 | integrin, beta 3 (platelet glycoprotein IIb, antigen CD61) [Homo sapiens] (Over 100 PubMed links)

Score = 1513 bits (3918), Expect = 0.0

Identities = 711/782 (90%), Positives = 751/782 (96%), Gaps = 0/782 (0%)

Query	6	PGQLWaalalgalagvvvgESNIC	TTRGVNSCQCLAVSPVCAWCSDE	TL	SQGS	PRCNL	65
		P LWA +LALGALAGV VG NICT	TTRGV+SCQCLAVSP+CAWCSDE	L	GS	PRC+L	
Sbjct	7	PRPLWATVLALGALAGVVGPNIC	TTRGVSSCQCLAVSPMCAWCSDE	AL	PLGS	PRCDL	66
Query	66	KENLLKDNCAPIESIEFPVSEAQ	ILEARPLSSKSGSSAQITQVSP	QRIALRLRPDDSKIF	125		
		KENLLKDNCAPIESIEFPVSEA++	LE RPLS KSGS S+Q+TQVSP	QRIALRLRPDDSK F			
Sbjct	67	KENLLKDNCAPIESIEFPVSEAR	VLEDRLPLSDKSGSDSQVTQVSP	QRIALRLRPDDSKNF	126		
Query	126	SLQVRQVEDYPVDIYYLMDLS	SFSMKDDLSSIQT	LGTKLASQMRKLT	NLRIGF	GAFVDKP	185
		S+QVRQVEDYPVDIYYLMDLS+	SMKDDL SIQ LGTKLA+QMRKLT	NLRIGF	GAFVDKP		
Sbjct	127	SIQVRQVEDYPVDIYYLMDLS	YSMKDDLWSIQNLG	TKLATQMRKLT	NLRIGF	GAFVDKP	186
Query	186	VSPYMYISPPQAIKNPCYNMKN	ACLPMFGYKHVLT	LT	DQVSRFNEEVKKQSVSRNR	DAPE	245
		VSPYMYISPP+A++NPCY+MK	CLPMFGYKHVLT	LT	DQV+RFNEEVKKQSVSRNR	DAPE	
Sbjct	187	VSPYMYISPPAALNCPYDMKT	TCLPMFGYKHVLT	LT	DQVTRFNEEVKKQSVSRNR	DAPE	246
Query	246	GGFDAIMQATVCDEKIGWRND	ASHLLVFTTDAKTHIALDGR	LAGIVLPNDGHCHIGTDNH	305		
		GGFDAIMQATVCDEKIGWRND	ASHLLVFTTDAKTHIALDGR	LAGIV PNDG CH+G+DNH			
Sbjct	247	GGFDAIMQATVCDEKIGWRND	ASHLLVFTTDAKTHIALDGR	LAGIVQPDGQCHVGSDNH	306		
Query	306	YSASTTMDYPSLGLMTEKLSQ	KNINLIFAVTENVVSLYQNY	SELIPGTTVGVLSD	SSNV	365	
		YSASTTMDYPSLGLMTEKLSQ	KNINLIFAVTENVV+LYQNY	SELIPGTTVGVL	S	SSNV	
Sbjct	307	YSASTTMDYPSLGLMTEKLSQ	KNINLIFAVTENVVNL	YQNYSELIPGTTVG	VL	SMDSSNV	366
Query	366	LQLIVDAYGKIRSKVEVRDL	PEELSLSFNATCLNNEV	IPGLKSCVGLKIGD	TVSFSIE	425	
		LQLIVDAYGKIRSKVEVRDL	PEELSLSFNATCLNNEV	IPGLKSC+GLKIGD	TVSFSIE		
Sbjct	367	LQLIVDAYGKIRSKVEVRDL	PEELSLSFNATCLNNEV	IPGLKSCMGLKIGD	TVSFSIE	426	
Query	426	AKVRGCPQEKEQSFTIKPVG	FKDSLTVQVTFDCDCACQ	AFAQPSSPRCNNGN	GT	FECGVC	485
		AKVRGCPQEKE+SFTIKPVG	FKDSL VQVTFDCDCACQ	A+P+S RCNNGN	GT	FECGVC	
Sbjct	427	AKVRGCPQEKEQSFTIKPVG	FKDSLIVQVTFDCDCACQ	AEPNSHRCNNGN	GT	FECGVC	486
Query	486	RCDQGWLGSMCESEEDYRPS	QQEECSPKEGQPICSQR	GECLCGQC	VCHSSDFGKITGKY	545	
		RC GWLGS CECSEEDYRPSQ	+ECSP+EGQP+CSQR	GECLCGQC	VCHSSDFGKITGKY		
Sbjct	487	RCGPGWLGSCCESEEDYRPS	QQDECS	PREGQPVCSQR	GECLCGQC	VCHSSDFGKITGKY	546
Query	546	CECDDFSCVRYKGEMCSGHG	QCNCGDCVCDSDWTGY	CNCTTRTDTCMSTN	GLLCSGRGN	605	
		CECDDFSCVRYKGEMCSGHG	QC+CGDC+CDSDWTGY	CNCTTRTDTCMS+NG	LLCSGRG		
Sbjct	547	CECDDFSCVRYKGEMCSGHG	QCSCGDCLCDSDWTGY	CNCTTRTDTCMSSN	GLLCSGRGK	606	
Query	606	CECGSCVCVQPGSYGDTCE	KCPTCPDACSFKKEC	VECKKFNRGTLHE	ENTCSRYCRDIE	665	
		CECGSCVC+QPGSYGDTCE	KCPTCPDAC+FKKEC	VECKKF+RG LH+ENTC	+RYCRD+IE		
Sbjct	607	CECGSCVCIQPGSYGDTCE	KCPTCPDACTFKKEC	VECKKFDRGALH	DENTCNRYCRDIE	666	

Query 666 QVKELTDTGKNAVNTYKNEDDCVVRFAQYYEDTSGRAVLVVEEPECCKGPDILVVLLSV 725
VKEL DTGK+AVNCTYKNEDDCVVRFAQYYED+SG+++LYVVEEPECCKGPDILVVLLSV
Sbjct 667 SVKELKDTGKDAVNCTYKNEDDCVVRFAQYYEDSSGKSILYVVEEPECCKGPDILVVLLSV 726

Query 726 MgailliglatlliwwllitiHDrkefakfeerarakWDANNPLYKEATSTFTNITYR 785
MGAILLIGLA LLIWKLLITIHDRKEFAKFEERARAKWDANNPLYKEATSTFTNITYR
Sbjct 727 MGAILLIGLAALLIWKLLITIHDRKEFAKFEERARAKWDANNPLYKEATSTFTNITYR 786

Query 786 GT 787
GT
Sbjct 787 GT 788

PAI-1: 78%

>ref|NP_000593.1| plasminogen activator inhibitor-1 [Homo sapiens]
Length=402

GENE ID: 5054 SERPINE1 | serpin peptidase inhibitor, clade E (nexin,
plasminogen activator inhibitor type 1), member 1 [Homo sapiens]
(Over 100 PubMed links)

Score = 630 bits (1626), Expect = 0.0
Identities = 316/402 (78%), Positives = 357/402 (88%), Gaps = 0/402 (0%)

```
Query 1  MQMSSALACLILGLVLVSGKGFTLPLRESHTAHQATDFGVKFQVQVQASKDRNVVFSKY 60
        MQMS AL CL+LGL LV G+G + S+ AH A+DFGV+VFQVQV QASKDRNVVFSKY
Sbjct 1  MQMSPALTCLVLGLALVFGGSAVHHPPSYVAHLASDFGVRVFQVQVQASKDRNVVFSKY 60

Query 61 GVSSVLAMLQMTTAGKTRRQIQDAMGFKVNEKGTAHALRQLSKELMGPWNKNEISTADAI 120
        GV+SVLAMLQ+TT G+T++QIQ AMGFK+++KG A ALR L KELMGPWNK+EIST DAI
Sbjct 61 GVASVLAMLQLTTGGETQQQIQAAAMGFKIDDKGMAPALRHLYKELMGPWNKDEISTDAI 120

Query 121 FVQRDLVLVQGFMPHFFKLFQTMVKQVDFSEVERARFIINDWVERHTKGMINDLLAKGAV 180
        FVQRDL+LVQGFMPHFF+LF++ VKQVDFSEVERARFIINDWV+ HTKGM++LL KGAV
Sbjct 121 FVQRDLKLVLQGFMPHFFRLFRSTVKQVDFSEVERARFIINDWVKTHTKGMISNLLKGAV 180

Query 181 DELTRLVLVNALYFSGQWKTPFLEASTHQRLFHKSDGSTVSPMMAQSNKFNYTEFTTPD 240
        D+LTRLVLVNALYF+GQWKTPF ++STH+RLFHKSDGSTVSPMMAQ+NKFNYTEFTTPD
Sbjct 181 DQLTRLVLVNALYFNGQWKTPFPDSSTHRRLLFHKSDGSTVSPMMAQTNKFNYTEFTTPD 240

Query 241 GLEYDVVELPYQRDTLSMFIAAPFEKDVHLSALTNILDAELIRQWKNMTRLPRLLILPK 300
        G YD++ELPY DTLSMFIAAP+EK+V LSALTNIL A+LI WKGNMTRLPRLL+LPK
Sbjct 241 GHYYDILELPYHGDTLSMFIAAPYEKEVPLSALTNILSAQLISHWKNMTRLPRLLVLPK 300

Query 301 FSLETEVDLRGPLEKLGMPDMFSATLADFTSLSDQEQLSVAQALQKVRIEVNESGTVASS 360
        FSLETEVDLR PLE LGM DMF ADFTSLSDQE L VAQALQKV+IEVNESGTVASS
Sbjct 301 FSLETEVDLRKPLENLGMTDMFRQFQADFTSLSDQEPLHVAQALQKVIEVNESGTVASS 360

Query 361 STAFVISARMAPTEMVIDRSFLFVVRHNPTETILFMGQVMEP 402
        STA ++SARMAP E+++DR FLFVVRHNPT T+LFMGQVMEP
Sbjct 361 STAVIVSARMAPEEIIMDRPFLFVVRHNPTGTVLFMGQVMEP 402
```

IL-4 Receptor: 52%

>emb|CAD12326.1| unnamed protein product [Homo sapiens]
emb|CAD28170.1| unnamed protein product [Homo sapiens]
emb|CAD28391.1| unnamed protein product [Homo sapiens]
emb|CAJ01243.1| unnamed protein product [Homo sapiens]
Length=825

Score = 799 bits (2064), Expect = 0.0

Identities = 427/816 (52%), Positives = 519/816 (63%), Gaps = 21/816 (2%)

```
Query 1  MGR LCTKFLTSVGCLILLV TCGSGSIKVLGEPTCFSDYIRTSTCEWFLDSA VDCSSQLCL 60
          MG LC+ L V CL+LL V SG++KVL EPTC SDY+ STCEW ++ +CS++L L
Sbjct 1  MGW LCGLLFPV SCLVLLQVASSGNMKVLQEPTCVSDYMSISTCEWKMGPTNCSTELRL 60

Query 61  HYRLMFFEFSENLTICIPRNSASTVCVCHMEMNRPVQSDRYQMELWAEHRQLWQGSFSPSG 120
          Y+L+F SE TCIP N+ CVCH+ M+ V +D Y ++LWA + LW+GSF PS
Sbjct 61  LYQLVFL-LSEAHTCIPENNGGAGCVCHLLMDDVVSADNYTLDLWAGQQLLWKGSFKPSE 119

Query 121  NVKPLAPDNLTLHTNVSEWLLTWNLYPSNNLLYKDLISMVNISREDNPAEFIVYNTY 180
          +VKP AP NLT+HTNVSD LLTW+N YP +N LY L VNI E++PA+F +YNTY
Sbjct 120  HVKPRAPGNLTVHTNVSDTLLLTWSNPYPDPNYLNLTYAVNIWSENDPADFRIYNTY 179

Query 181  KEPRLSFPINILMSGVYYTARVRVRSQILTGTWSEWSPSITWYNHQPLIQLPLGVTI 240
          EP L + L SG+ Y ARVR +Q TWSEWSPS W+N ++ P Q L LGV++
Sbjct 180  LEPSLRIAATLKS GISYRARVRAWAQCYN TTWSEWSPSTKWHNSYREPFEQHLLLGVS V 239

Query 241  SCLCIPLFLCFYCSITKIKKIWW DQIPTPARSPLVAII IQDAQVPLWDKQTRSQUESTKY 300
          SC+ I CL CY SITKIKK WWDQIP PARS LVAII IQDAQ W+K++R QE K
Sbjct 240  SCIVILAVCLLCYVSITKIKKEWWDQIPNPARSRLVAII IQDAQSGWEKRSRQEPAPKC 299

Query 301  PHWKTCLDKLLPCLLKHVRKKKTD FPKAAPT KSLQSPGKAGWCPMEVSRTVLWPENVSVS 360
          PHWK CL KLLPC L+H +K+ D KAA Q GK+ WCP+E+S+TVLWPE S+S
Sbjct 300  PHWKNCLTKLLPCFLEHNMKRDEDPHKA AKEMPFQSGKSAWCPVEISKTVLWPE--SIS 357

Query 361  VVRCMELFeapvqnveeeedeivkeDLSMSPENSGGCGFQESQADIMARLTENLFSDDLLE 420
          VVRC+ELFEAPV+ EEEE E K SPE+S FQE + I+ARL TE+LF DLL
Sbjct 358  VVRCVELFEAPVECEEEEEVEEEKGSFCASPESSRD-DFQEGREGI VARLTESLFDLLG 416

Query 421  AENGGLGQSALAESCSPLPSGSGQASVSWACLPMPGSEEATCQVTEQPSH--PGPLSGSP 478
          ENGG Q + ESC PSGS A + W P +EA EQP H P P SP
Sbjct 417  EENG GFCQQDMGESCLLP SGSTSAHMPWDEFPSAGPKEAPPWGKEQPLHLEPSP-PASP 475

Query 479  AQSAPTLACTQVPLVLADNPAYRSFSDCCSPAPNPGELAPEQQQADHLEEEEPSPADPH 538
          QS L CT+ PLV+A NPAYRSFS+ S +P P EL P+ A HLEE EP P P
Sbjct 476  TQSPDNLCTETPLVIAGNPAYRSFSNSLSQSPCPRELGPDP LLARHLEEEVEPEMPCVPQ 535

Query 539  SSGP---PMQPVESWEQILHMSVLQHgaagstpapaggYQEFVQAVKQGA AQDPGVPGV 595
          S P P E+WEQIL +VLQHGA AA AP GYQEFV AV+QG Q V G+
Sbjct 536  LSEPTTVPQPEPETWEQILRRNVLQHGA AAAPVSAPTSGYQEFVHAVEQGGTQASAVVGL 595

Query 596  RPSGDPGYKAFSSLLSSNGIRgdt aaagtd dghggYKPFqnpvp----nqspssvpLFTF 651
          P G+ GYKAFSSLL+S+ + + G G GYKPFQ+ +P + +P VPLFTF
Sbjct 596  GPPGEAGYKAFSSLLASSAVSPEKCGFGASSGEEGYKPFQDLIPGCPGDPAPVPVPLFTF 655
```

Query 652 GLDTELSPLNSDPPKSPPEClglelgkkgDWVKAPPPADQVPKPFGDDLGFIVYSS 711
 GLD E SP +S P S PE LGLE G K D K P P +Q P D LG GIVYS+
 Sbjct 656 GLDREPPRSPQSSHLPSSSPEHLGLEPGEKVEDMPKPPLPQEQATDPLVDSLCSGIVYSA 715

Query 712 LTCHLCGHLKQHHSQEEGGQSPIVASPGCCCYDDRSPLGSLSGALESCPEGIPPEANL 771
 LTCHLCGHLKQ H QE+GGQ+P++ASP CGCC DRS + A + P G+P EA+L
 Sbjct 716 LTCHLCGHLKQCHGQEDGGQTPVMASPGCCCGDRSSPPTPLRAPDPSPGGVPLEASL 775

Query 772 MSAPKTPSNLSGEGK-----GPGHSPVPSQTTEV 800
 A PS +S + K PG++ SQT ++
 Sbjct 776 CPASLAPSGISEKSKSSSSFHPAPGNAQSSSQTPKI 811

IL-5 Receptor: 68%

>ref|NP_000555.2| interleukin 5 receptor, alpha isoform 1 precursor [Homo sapiens]
ref|NP_783853.1| interleukin 5 receptor, alpha isoform 1 precursor [Homo sapiens]
Length=420

GENE ID: 3568 IL5RA | interleukin 5 receptor, alpha [Homo sapiens]
(Over 10 PubMed links)

Score = 584 bits (1505), Expect = 5e-167
Identities = 285/414 (68%), Positives = 335/414 (80%), Gaps = 2/414 (0%)

```
Query 4  VLLILVGALATLQADLLNHKKFLLLPVNFTIKATGLAQVLLHWDPNPDQEQRHVDLEYH 63
          VLLIL+GA LQADLL +K LLPPVNFTIK TGLAQVLL W PNPDQEQR+V+LEY
Sbjct 7  VLLIILLGATEILQADLLPDEKISLLPPVNFTIKVTGLAQVLLQWKPNPDQEQRVNLEYQ 66

Query 64  VKINAPQEDEYDTRKTESKCVTPLHEGFAASVRTILKSSHTTLASSWVS AELKAPPGSPG 123
          VKINAP+ED+Y+TR TESKCVT LH+GF+ASVRTIL++ H+ LASSW SAEL APPGSPG
Sbjct 67  VKINAPKEDDYETRITESKCVTILHKGFSAASVRTILQNDHSSLASSWASAELHAPPGSPG 126

Query 124  TSVTNLTCTtthtvsshthLRPYQVSLRCTLVVGKDAPEDTQYFLYYRFGVLTEKCQEYS 183
          TS+ NLCTT+T +++ LR YQVSL CTWLVG DAPEDTQYFLYYR+G TE+CQEYS
Sbjct 127  TSIVNLCTTNTTEDNYSRLRSYQVSLHCTLVVGTDAPEDTQYFLYYRGSWTEECQEYS 186

Query 184  RDALNRNTACWFPRTFINSKGFEQLAVHINGSSKRAAIKPFQQLFSPLAIDQVNPPRNV 243
          +D L RN ACWFPRTFI SKG + LAV +NGSSK +AI+PFDQLF+ AIDQ+NPP NVT
Sbjct 187  KDTLGRNIACWFPRTFILSKGRDWLAVLVNGSSKHSAIRPFDQLFALHAIDQINPPLNVT 246

Query 244  VEIESNSLYIQWEKPLSAFPDHCIFYELKIYNTKNGHIQKEKLIANKFISKIDDVSTYSI 303
          EIE L IQWEKP+SAFP HCF+YE+KI+NT+NG++Q EKL+ N FIS IDD+S Y +
Sbjct 247  AEIEGTRLSIQWEKPVSAFPIHCFDYEVIHNTRNGYLQIEKLMTNAFISIIDDLSKYDV 306

Query 304  QVRAAVSSPCRMPCRWGEWSQPIYVGK-ERKSLVEWHLIVLPTAACFVLLIFSLICRVCH 362
          QVRAAVSS CR G W EWSQPIYVG E K L EW +IV+ CF+LLI SLIC++CH
Sbjct 307  QVRAAVSSMCREAGLWSEWSQPIYVGNDHKLPLREWFVIVIMATICFILLILSLICKICH 366

Query 363  LWTRLFPPVPAPKSNIKDLPVVTEYEKP-SNETKIEVVHCVVEVGFEVMGNSTF 415
          LW +LFPP+PAPKSNIKDL V T YEK S+ET+IEV+ +E+ G E + +S F
Sbjct 367  LWIKLFPPIPAPKSNIKDLFVTTNYEKAGSSETEIEVICYIEKPGVETLEDVSF 420
```


Eotaxin Receptor: 70%

>ref|NP_001828.1| CC chemokine receptor 3 [Homo sapiens]

ref|NP_847899.1| CC chemokine receptor 3 [Homo sapiens]

Length=355

GENE ID: 1232 CCR3 | chemokine (C-C motif) receptor 3 [Homo sapiens]

(Over 10 PubMed links)

Score = 503 bits (1294), Expect = 1e-142

Identities = 244/348 (70%), Positives = 287/348 (82%), Gaps = 0/348 (0%)

```
Query 12  VESFETTPYEYEWAPPCEKVRIKELGSWLLPPLYSLVFIIGLLGNMMVVLILIKYRKLQI 71
          VE+F TT Y + CEK + L + +PPLYSLVF +GLGN++VV+ILIKYR+L+I
Sbjct 8   VETFGTTSYDDVGLLCEKADTRALMAQFVPPPLYSLVFTVGLGNVVVVMILIKYRRLRI 67

Query 72  MTNIYLFNLAISDLLFLFTVPFVIHYVLWNEWGFGHYMCKMLSGFYLYALYSEIFFIILL 131
          MTNIYL NLAISDLLFL T+PFIHYV + W FGH MCK+LSGFY+ LYSEIFFIILL
Sbjct 68  MTNIYLLNLAISDLLFLVTLPFVIHYVRGNWVFGHGMCKLLSGFYHTGLYSEIFFIILL 127

Query 132 TIDRYLAIVHAVFALRARTVTFATITSIITWGLAGLAALPEFIFHESQDSFGEFSCSPRY 191
          TIDRYLAIVHAVFALRARTVTF ITSI+TWGLA LAALPEFIF+E+++ F E CS Y
Sbjct 128 TIDRYLAIVHAVFALRARTVTFGVITSIVTWGLAVLAALPEFIFYETEELFEETLCSALY 187

Query 192 PEGEEDSWKRFHALRMNIFGLALPLLIMVICYSGIIKTLRCPNKKKKHAIRLifvmmiv 251
          PE SW+ FH LRM IF L LPLL+M ICY+GIKTLRCP+KKK+KAIRLIFV+M V
Sbjct 188 PEDTVYSWRHFHTLRMTIFCLVPLLVMAICYTGIIKTLRCPSSKKKYKAIRLIFVIMAV 247

Query 252 fffFWTPYNLVLLFSAFHSTFLETSCQSKHLDLAMOQTEVIAYTHCCINPVIYAFVGEr 311
          FFIFFWTPYN+ +L S++ S C++SKHLDL M VTEVIAY+HCC+NPVIYAFVGER
Sbjct 248 FFIFFWTPYNVAILLSSYQSILFGNDCERSKHLDLVMVTEVIAYSHCCMNPVIYAFVGER 307

Query 312 frkhlrlffhrNVAVYLGKYIPFLPGEKMERTSSVSPSTGEQEISVVF 359
          FRK+LR FFHR++ ++LG+YIPFLP EK+ERTSSVSPST E E+S+VF
Sbjct 308 FRKYLRFHFHRHLLMHLGRYIPFLPSEKLERTSSVSPSTAEPELSIVF 355
```

PDGF β Receptor: 85%

>ref|NP_002600.1| platelet-derived growth factor receptor beta precursor [Homo sapiens]
Length=1106

GENE ID: 5159 PDGFRB | platelet-derived growth factor receptor, beta polypeptide [Homo sapiens] (Over 100 PubMed links)

Score = 1915 bits (4962), Expect = 0.0

Identities = 944/1106 (85%), Positives = 1021/1106 (92%), Gaps = 8/1106 (0%)

Query	1	MGLPGVIPAlvIrgql11-svlw11GPQTSRGLVITPPGPEFVLNISSTFVLTCSGSAPV	59
		M LPG +PAL L+G+LLL S+L LL PQ S+GLV+TPPGPE VLN+SSTFVLTCSGSAPV	
Sbjct	1	MRLPGAMPALALKGELLLL SLLLLLEPQISQGLVVTTPGPELVNVSSTFVLTCSGSAPV	60
Query	60	MWEQMSQVPWQEAAMNQDGTFSVLTLTNVTGGDTGEYFCVYNNSLGPELSERKRIYIFV	119
		+WE+MSQ P QE A QDGTFSVLTLTN+TG DTGEYFC +N+S G E ERKR+YIFV	
Sbjct	61	VWERMSQEPPEMAKAQDGTFSVLTLTNLTGLDTGEYFCTHNSRGLTDERKRLYIFV	120
Query	120	PDPTMGFLPMDSEDLFIFVTDVTETTIPCRVTD PQLEVTLHEKKVDIPLHVPYDHQRGFT	179
		PDPT+GFLP D+E+LFIF+T++TE TIPCRVTD PQ VTLHEKK D+ L VPYDHQRGF+	
Sbjct	121	PDPTVGFLPNDAEELFIFLTEITEITIPCRVTD PQLVTLHEKKGDVALPVPYDHQRGFS	180
Query	180	GTFEDKTYICKTTIGDREVDSDTYVYVSLQVSSINVSNAVQTVVRQGESITIRCIVMGN	239
		G FED++YICKTTIGDREVDSD YVYV LQVSSINVSNAVQTVVRQGE+IT+ CIV+GN	
Sbjct	181	GIFEDRSYICKTTIGDREVDSDAYVYVRLQVSSINVSNAVQTVVRQGENITLMCIVIGN	240
Query	240	DVVNFQWYTPRMKSGRLVEPVDYLFVGVPSRIGSILHIPTAELSDSGTYTCNVSVSNDH	299
		+VVNF+WYTPR +SGRLVEPVD+L +P I SILHIP+AEL DSGTYTCNV+ SVNDH	
Sbjct	241	EVVNFQWYTPRMKSGRLVEPVDYLFVGVPSRIGSILHIPTAELSDSGTYTCNVSVSNDH	300
Query	300	GDEKAINISVIENG YVRLLETGLDVEIAELHRSRTL RVVFEAYPMP SVLWLDNRTL GDS	359
		DEKAINI+V+E+GYVRL +G ++ AELHRSRTL+VVFEAYP P+VLW KDNRTL GDS	
Sbjct	301	QDEKAINITVVEG YVRLLEGEVGLQFAELHRSRTL QVVFEAYP PPTVLWFDNRTL GDS	360
Query	360	GAGELVLSTRNMSETRYVSELILVRVKVSEAGYYTMRAFHEDEVLQSFKLQVNPVRVL	419
		AGE+ LSTRN+SETRYVSEL LVRVKV+EAG+YTMRAFHEDE VLQSF+LQ+NVPVRVL	
Sbjct	361	SAGEIALSTRNMSETRYVSELILVRVKVAEAGHYTMRAFHEDEVLQSFKLQVNPVRVL	420
Query	420	ELSESHPANGEQTIRCRGRMPQPNVTWSTCRDLKRCPRKLSPTPLGNSSEESQLETNV	479
		ELSESHP +GEQT+RCRGRMPQPN+ WS CRDLKRCPR+L PT LGNSS+EESQLETNV	
Sbjct	421	ELSESHPDSEGT VRCRGRMPQPN IWSACRDLKRCPRELPPTLLGNSSEESQLETNV	480
Query	480	TFWEEDQEYEVVSTLRLRHVDQPLSVRCMLQNSMGDSQEVTVVPHSLPFKVVVISAILA	539
		T+WEE+QE+EVVSTLRL+HVD+PLSVRC L+N++G D+QEV VVPHSLPFKVVVISAILA	
Sbjct	481	TYWEEEQEFVSTLRLRHVDQPLSVRCMLQNSMGDSQEVTVVPHSLPFKVVVISAILA	540
Query	540	lvvltvisliilimlwqkkpryeirwkviesvssdgheyiyvdpvqlpydstwelprdqL	599
		LVLTL+ISLIILIMLWQKKPRYEIRWKVIESVSSDGHEYIYVDP+QLPYDSTWELPRDQL	
Sbjct	541	LVLTLIISLIILIMLWQKKPRYEIRWKVIESVSSDGHEYIYVDPMLPYDSTWELPRDQL	600
Query	600	VLGRTLGSAGFQVVEATAHGLSHSQATMKVAVKMLKSTARSSSEKQALMSELKIMSHLGP	659
		VLGRTLGSAGFQVVEATAHGLSHSQATMKVAVKMLKSTARSSSEKQALMSELKIMSHLGP	
Sbjct	601	VLGRTLGSAGFQVVEATAHGLSHSQATMKVAVKMLKSTARSSSEKQALMSELKIMSHLGP	660

Query	660	HLNVNLLGACTKGGPIYIITEYCRYGDLVDYLHRNKHTFLQRHSNKHCPPSAELYSNAL	719
		HLNVNLLGACTKGGPIYIITEYCRYGDLVDYLHRNKHTFLQ HS+K PPSAELYSNAL	
Sbjct	661	HLNVNLLGACTKGGPIYIITEYCRYGDLVDYLHRNKHTFLQHSDKRRPPSAELYSNAL	720
Query	720	PVGFSPLSHLNLTGESDGGYDMSKDESIDYVPM LDMKGD IKYADIESPSYMAPYDNYVP	779
		PVG LPSH++LTGESDGGYDMSKDES+DYVPM LDMKGD+KYADIES +YMAPYDNYVP	
Sbjct	721	PVGLPLPSHVS LTGESDGGYDMSKDESVDYVPM LDMKGDVKYADIESSNYMAPYDNYVP	780
Query	780	SAPERTYRATLINDSPVLSYTDLVGFSYQVANGMDFLASKNCVHRDLAARNVLICEGKLV	839
		SAPERT RATLIN+SPVLSY DLVGFSYQVANGM+FLASKNCVHRDLAARNVLICEGKLV	
Sbjct	781	SAPERTCRATLINESPVLSYMDLVGFSYQVANGMEFLASKNCVHRDLAARNVLICEGKLV	840
Query	840	KICDFGLARDIMRDSNYISKGSTYLPLKWMAPESIFNSLYTTLSDVWSFGILLWEIFTLG	899
		KICDFGLARDIMRDSNYISKGST+LPLKWMAPESIFNSLYTTLSDVWSFGILLWEIFTLG	
Sbjct	841	KICDFGLARDIMRDSNYISKGSTFLPLKWMAPESIFNSLYTTLSDVWSFGILLWEIFTLG	900
Query	900	GTPYPELPMNDQFYNAIKRGYRMAQPAHASDEIYEIMQKCWEEKFETRPPFSQlvlller	959
		GTPYPELPMN+QFYNAIKRGYRMAQPAHASDEIYEIMQKCWEEKFE RPPFSQLVLLLER	
Sbjct	901	GTPYPELPMNEQFYNAIKRGYRMAQPAHASDEIYEIMQKCWEEKFEIRPPFSQLVLLLER	960
Query	960	llgegYKKKYQQVDEEFLRSDHPAILRSQARFPGIHSLSPLDTSSVLYTAVQPNE SDND	1019
		LLGEGYKKKYQQVDEEFLRSDHPAILRSQAR PG H LRSPLDTSSVLYTAVQPNE DND	
Sbjct	961	LLGEGYKKKYQQVDEEFLRSDHPAILRSQARLPGFHLSPLDTSSVLYTAVQPNEG DND	1020
Query	1020	YIIPLDPKPDVADEGLPEGSPSLASSTLNEVNTSSTISCDSplelqeepp-----qa	1072
		YIIPLDPKPDVADEG EGSPSLASSTLNEVNTSSTISCDSPLE Q+EP+ Q	
Sbjct	1021	YIIPLDPKPEVADEGPLEGSPSLASSTLNEVNTSSTISCDSPLEQDEPEPEPQLELQV	1080
Query	1073	epeaqleqpqDSGCPGLAEADSFL	1098
		EPE +LEQ DSGCP P AEADSFL	
Sbjct	1081	EPEPELEQLPDSGCPAPRAEADSFL	1106

α V β 3 Integrin: 92%

>ref|NP_002201.1| integrin alpha-V precursor [Homo sapiens]
Length=1048

GENE ID: 3685 ITGAV | integrin, alpha V (vitronectin receptor, alpha polypeptide, antigen CD51) [Homo sapiens] (Over 100 PubMed links)

Score = 1964 bits (5087), Expect = 0.0

Identities = 968/1049 (92%), Positives = 1008/1049 (96%), Gaps = 6/1049 (0%)

Query	1	MAApgrlllrprpggl1111pglllplADAFNLDVESPAEYAGPEGSYFGFAVDFFEPST	60
		MA P R LR P GL LLL GLLPL AFNLDV+SPA EY+GPEGSYFGFAVDFF PS	
Sbjct	1	MAFPpRRRLRLGPRGLPLLLSGLLLPLCRAFNLVDSPA EYSGPEGSYFGFAVDFFVPSA	60
Query	61	SSRMFLLVGAPKANTTQPGIVEGGQVLKCECSSRRQCPIEFDSTGNRDYAKDDPLEFKS	120
		SSRMFLLVGAPKANTTQPGIVEGGQVLK+ SS+RRQCPIEFD+TGNRDYAKDDPLEFKS	
Sbjct	61	SSRMFLLVGAPKANTTQPGIVEGGQVLKCDWSSTRQCPIEFDATGNRDYAKDDPLEFKS	120
Query	121	HQWFGASVRSKQDKILACAPLYHWRTMKQEREPVGTCLQDGTKTVEYAPCRSKNIDAD	180
		HQWFGASVRSKQDKILACAPLYHWRTMKQEREPVGTCLQDGTKTVEYAPCRS++IDAD	
Sbjct	121	HQWFGASVRSKQDKILACAPLYHWRTMKQEREPVGTCLQDGTKTVEYAPCRSQDIDAD	180
Query	181	GQGFCCGGFSIDFTKADRVLLGGPGSFYWQGLISDQVAEIISKYDPNVYSIKYNNQLAT	240
		GQGFCCGGFSIDFTKADRVLLGGPGSFYWQGLISDQVAEI+SKYDPNVYSIKYNNQLAT	
Sbjct	181	GQGFCCGGFSIDFTKADRVLLGGPGSFYWQGLISDQVAEIVSKYDPNVYSIKYNNQLAT	240
Query	241	RTAQAIFFDSYLGSYAVGDFNGDGIEDFVSGVPRAARTLGMVYIYDGKNMSSLHNFTGE	300
		RTAQAIFFDSYLGSYAVGDFNGDGI+DFVSGVPRAARTLGMVYIYDGKNMSSL+NFTGE	
Sbjct	241	RTAQAIFFDSYLGSYAVGDFNGDGIIDFVSGVPRAARTLGMVYIYDGKNMSSLYNFTGE	300
Query	301	QMAAYFGFSVAATDINGDDYADVFIGAPLFMDRGSDGKLQEVGQVSVSLQRAVGDFQTTK	360
		QMAAYFGFSVAATDINGDDYADVFIGAPLFMDRGSDGKLQEVGQVSVSLQRA GDFQTTK	
Sbjct	301	QMAAYFGFSVAATDINGDDYADVFIGAPLFMDRGSDGKLQEVGQVSVSLQRASGDFQTTK	360
Query	361	LNGFEVFARFGSAIAPLGDLDDQDGFNDIAIAAPYGGEDKKGLVYIFNGRSTGLNSVPSQI	420
		LNGFEVFARFGSAIAPLGDLDDQDGFNDIAIAAPYGGEDKKG+VYIFNGRSTGLN+VPSQI	
Sbjct	361	LNGFEVFARFGSAIAPLGDLDDQDGFNDIAIAAPYGGEDKKGIVYIFNGRSTGLNAVPSQI	420
Query	421	LEGQWAAQSMPPSFGYSMKGATDVDRNGYPDLVVGAFGVDRVLYRARPVTVNAGLEVY	480
		LEGQWAA+SMPPSFGYSMKGATD+D+NGYPDL+VGAFGVDR+LYRARPV+TVNAGLEVY	
Sbjct	421	LEGQWAARSMPSPFGYSMKGATDIDKNGYPDLIVGAFGVDRVLYRARPVITVNAGLEVY	480
Query	481	PSILNQDNKICPLPGTALKVSCFNVRFLKADGKGLPRKLHFQVELLLDKLKQKGAIRR	540
		PSILNQDNK C LPGTALKVSCFNVRFLKADGKG LPRKL+FQVELLLDKLKQKGAIRR	
Sbjct	481	PSILNQDNKTCSLPGTALKVSCFNVRFLKADGKGVLPRLNHFQVELLLDKLKQKGAIRR	540
Query	541	ALFLHNRSPPVHSKTMVFRGGQMCEELVAYLRDESEFRDKLTPITIFMEYRLDQRTAAD	600
		ALFL++RSP HSK MT+ RGG MQCEEL+AYLRDESEFRDKLTPITIFMEYRLD RTAAD	
Sbjct	541	ALFLYSRSPSHSKNMTISRGGLMQCEELIAYLRDESEFRDKLTPITIFMEYRLDYRTAAD	600
Query	601	ATGLQPILNQFTPANVSRQAHILLDCGEDNVCKPKLEVSVNSDQKKIYIGDDNPLTLTVK	660
		TGLQPILNQFTPAN+SRQAHILLDCGEDNVCKPKLEVSV+SDQKKIYIGDDNPLTL VK	
Sbjct	601	TTGLQPILNQFTPANISRQAHILLDCGEDNVCKPKLEVSVSDQKKIYIGDDNPLTLIVK	660

Query	661	AQNQGEGAYEAEIVSIPQADFIGVVRNNEALARLSCAFKTENQTRQVVC DLGNPMKAG	720
		AQNQGEGAYEAEIVSIP QADFIGVVRNNEALARLSCAFKTENQTRQVVC DLGNPMKAG	
Sbjct	661	AQNQGEGAYEAEIVSIPLQADFIGVVRNNEALARLSCAFKTENQTRQVVC DLGNPMKAG	720
Query	721	TQLLAGLRFSVHQSEMDTSVKFDLKIQSSNSFDNVSPVVS YKVDLAVLA AVEIRGVSSP	780
		TQLLAGLRFSVHQSEMDTSVKFDL+IQSSN FD VSPVVS+KVDLAVLA AVEIRGVSSP	
Sbjct	721	TQLLAGLRFSVHQSEMDTSVKFDLKIQSSNLFDKVSPVVS HKVDLAVLA AVEIRGVSSP	780
Query	781	DHIFLPIPNWEYKENPETEEDVGPIVQHIYELRNNGPSSFSKAILNLQWPKYNNNTLLY	840
		DHIFLPIPNWE+KENPETEEDVGP+VQHIYELRNNGPSSFSKA+L+LQWPKYNNNTLLY	
Sbjct	781	DHIFLPIPNWEHKENPETEEDVGPVVQHIYELRNNGPSSFSKAMLHLQWPKYNNNTLLY	840
Query	841	ILHYDIDGPMNCTADTEINPLRIK-----TPEKNDTAAAGQGERNHLITKRDLTLREGDV	895
		ILHYDIDGPMNCT+D EINPLRIK T EKNDT AGQGER+HLITKRDL L EGD+	
Sbjct	841	ILHYDIDGPMNCTSDMEINPLRIKISSLOTTEKNDT-VAGQGERDHLITKRDLALSEGDI	899
Query	896	HTLGCGIAKCLQITCQVGRLDRGKSAILYVKSLLWTETFMNKENQNHYSYSLKSSASFNI I	955
		HTLGCG+A+CL+I CQVGRLDRGKSAILYVKSLLWTETFMNKENQNHYSYSLKSSASFN+I	
Sbjct	900	HTLGCGVAQCLKIVCQVGRLDRGKSAILYVKSLLWTETFMNKENQNHYSYSLKSSASFNVI	959
Query	956	EFPYKNLPIDELFNSTLVTTNITWGIQAPAMPVPVWV IILAVLAGL LLLAVLVFVMYRMG	1015
		EFPYKNLPID+ NSTLVTTN+TWGIQAPAMPVPVWV IILAVLAGL LLLAVLVFVMYRMG	
Sbjct	960	EFPYKNLPIDITNSTLVTTNVTWGIQAPAMPVPVWV IILAVLAGL LLLAVLVFVMYRMG	1019
Query	1016	FFKrvrppqeeqereqlqPHENGEGNSET	1044
		FFKRVRPPQEEQEREQLQPHENGEGNSET	
Sbjct	1020	FFKRVRPPQEEQEREQLQPHENGEGNSET	1048